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EMBL; X62671; CAA44545.1; ALT_INIT.
EMBL; X62671; CAA44545.1; ALT_INIT.
EMBL; X65922; CAA46715.1; ALT_INIT.
EMBL; D26610; BAA05655.1; ALT_INIT.
EMBL; D25610; BAA05655.1; ALT_INIT.
EMBL; D3715; AAA91564.1; ALT_INIT.
EMBL; U31499; AAA83776.1; ALT_INIT.
EMBL; U712543; AAB53915.1; ALT_INIT.
EMBL; U72543; AAB53915.1; ALT_INIT.
                                                                                                    P49689; 082203; Q9M0E4;
01-FEB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
405 ribosomal protein s30.
(RPS30A OR AT2G19750 OR F6F22.22) AND
(RPS30B OR AT4G29390 OR F17A13.210) AND
(RPS30C OR AT5G56670 OR MIK19.12).
                                                       Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE 59 AA; 6648
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Submitted (DEC-1995) t
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Rossman T.G., Wang
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HGNC:3597; FAU.
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Pred. No. 2.2e-53;
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EX Lobas M., Regad F., Lacoure B.;

EX SIZIENCE FROM NA., RPS30A).

RC STRAINS—2003348; PubMed=106;719;

RX MEDITHR=200348; PubMed=106;719;

RX MEDITHR=200348; PubMed=106;719;

RA LIA X. Kaul S., Rounsley S.D., Shea T.P., Benito M.-T., Town C.D., RA LIA X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-T., Town C.D., RA LIA X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-T., Town C.D., RA LIA X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-T., Town C.D., RA LIA X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-T., Town C.D., RA LIA X., Kaul S., Rounsley S.D., Shea T.P., Benito M., Coreasy T.H., RA LIA X., Kaul S., Rounsley S.D., Shea T.P., Benito M., Coreasy T.H., RA LIA X., Kaul S., Rounsley S.D., Shea T.P., Benito M., Coreasy T.H., RA LIA X., Kaul M., Pali G., Ven Aken S. Y., Walland K.S., Croul S., Lee J.J., Rounsley G., Ven Aken S., Croul S., Ra Lia X., Shen M., Pali G., Ven Aken S., Unayam L., Ra Rounsley S., Ra Lia X., Shen M., Pali G., Ven Aken S., Croul S., Ra Lia X., Shen M., Pali G., Ven Aken S., Ra Lia X., Shen M., Pali G., Ven Aken S., Croul S., Ra Lia X., Shen M., Ra Lia X., Shen M., Ra Lia X., Ra Lia X
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EMBL; AC005169; AAC62141.2; --
EMBL; AL61574; CAB79697.1; --
EMBL; AL096692; --; NOT_ANNOTATED_CDS.
EMBL; AB01392; BAB09885.1; --
EMBL; AV062341; AAK96533.1; --
EMBL; AY061910; AAL31237.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by t SSP consortium (Salk/Stanford/PGEC)."; SSP consortium (Salk/Stanford/PGEC)."; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases. Submitted (CCT-2001) to THE S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                              "An in situ hybridization screen for the rapid isolation of differentially expressed genes.";

Dev. Genes Evol. 210:28-33(2000).

-I- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN.

-I- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                      Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
40S ribosomal protein S30.
FAU OR RPS30.
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                                                                                                                                                                                                                         MEDLINE=20070552; PubMed=10603084;
Henrich T., Wittbrodt J.;
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CONFLICT
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              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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RESULT 5
RS30_SCHPO STANDARD; PRT; 61 AA.

ID RS30_SCHPO STANDARD; PRT; 61 AA.

AC 042952; 014314;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S30.
GN (RPS30A OR RPS50 OR SPAC19B12.04) OR (RPS30B OR SPBC19G7.03C).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC Schizosaccharomycetales; Schizosaccharomycetes;
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Matches 12
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Best Local Similarity
Matches 18; Conserv
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L., Koonin E.V., Shallom S., Mason T., Yu K., Fylli C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertee M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O. Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS30_PLAFA 096269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ238274; CAB40969.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40S ribosomal protein RPS30 OR PFB0885W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seg
30-MAY-2000 (Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001422; AAC71966.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 282:1126-1132(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99021743; PubMed-9804551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 QYNRRFVNVVPTFGKKKG
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                                                                                                                                                                                                                                                  1 KVHGSLARAGKV 12
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                                                                                                                                                                                                                        KVHGSLARAGKV
                                                                                                                                                                                                                                                                                    12;
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59 AA;
                                                                                                                                                                                                                                                                                                                                              protein.
58 AA; 6488 MW;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                               525675AE74D04E5F CRC64;
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1.4e-05;
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1.1e-11
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RESULT 6
RS30_YEAST
ID RS30_Y
AC Q12087
DT 01-NOV
DT 01-NOV
DT 15-DEC
DE 40S r1
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                                                                                                                                                                                                                                                                                          Query Match
Best Local
                 RS30_YEAST
Q12087;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1998
                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lenaers G., Perret E.,
                                                                                                 3 KVHGSLARAGKV 14
                                                                                                                   1 KVHGSLARAGKV
         ribosomaı
                                                                                                                                                                                       AL390814; CAC00552.1; AL021839; CAA17057.2;
                                                                                                                                                                                                          AJ002731; CAA05693.1; -.
                                                                                                                                     l Similarity
12; Conserv
                                                                                                                                                                        protein;
61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gwilliam
(Rel. 35, Creaceu,
(Rel. 35, Last sequence update)
(Rel. 37, Last annotation update)
wal protein S30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tion of ribosomal genes is down regulated in fission yeast.";
                                                                                                                                    Conservative
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽.,
                                                                                                                                                                        Multigene
6910 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RPS30A AND RPS30B).
                                                                                                                                             20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rajandream M.A., Lyne M., Lyne R.,
                                                                                                                                    0
                                                                                                                                            Score 12;
Pred. No.
                                                                                                                                                                     family.
4B9C171F1A326F22 CRC64;
                                                                                                                                                                                                                                                                                        WO GENES FOR S30 IN S.POMBE.
S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                    Mismatches
                                                     62
                                                                                                                                   1.4e-05;
hes 0;
                                                                                                                                                     DB 1;
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                                                                                                                                                   Length 61;
                                                                                                                                   Indels
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RESULT
RS30_ON
ID RS
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AC P8
DT 15
DT 15
DT 15
CG GN FA
OS Or
OC EU
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Best Local
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EMBL; U48699; AAC49316.1; --
EMBL; U83406; AAB41050.1; --
EMBL; U83407; AAB41051.1; --
EMBL; U17243; AAB67333.1; --
EMBL; 275090; CAA99391.1; --
                                                                            RS30_ONCMY
P83328;
15-JUN-2002
15-JUN-2002
15-JUN-2002
 Eukaryota; Metazoa; Actinopterygii; Neop
                                Oncorhynchus mykiss
                                                                                                                                                             ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hughes B., Pohl T.M.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

-i- MASS SPECTROMETRY: MW-6987; MW_ERR-3.4; METHOD-MALDI.

-i- MISCELLANEOUS: THERE ARE TWO GENES FOR S30 IN YEAST.

-i- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Favello A., Fulton L., Gattung S., Greco T., Kirsten J., K Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Miller N., Nhan M., Pauley A., Peluso D., Rikken L., Riles Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Submitter A., Naterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (RPS30B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker R.T., Williamson N.A., Wettenhall R.E.H.;
"The yeast homolog of mammalian ribosomal protein S30 is expressed from a duplicated gene without a ubiquitin-like protein fusion sequence. Evolutionary implications.";
J. Biol. Chem. 271:13549-13555(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetaes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE (RPS30A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RPS30A OR YLR287BC OR L8003.23) AND (RPS30B OR YOR182C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             1 KVHGSLARAGKV 12
                                                                                                                                                                                                                           N
                                                          JUN-2002 (Rel. 41, Created)
JUN-2002 (Rel. 41, Last sequence up
JUN-2002 (Rel. 41, Last annotation
ribosomal protein S30 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                               S0004278; RPS30A.
S0005708; RPS30B.
                                                                                                                                                                                                                         KVHGSLARAGKV
                                                                                                                                                                                                                                                                                      l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                             STANDARD;
kiss (Rainbow trout) (Salmo gairdneri)
zoa; Chordata; Craniata; Vertebrata; El
Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                   6987 MW;
                                                                                                                                                                                                                                                                                    20.3%; So
100.0%; I
tive 0;
                                                                                                                                                                                                                                                                                                 Score 12;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                  65EADAED8D9FC586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               family.
                                                                                                                                                                                                                                                                                    Mismatches
                                                                            update)
                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                    1.4e-05;
                                                                                                                                                                                                                                                                                                                 Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson D.,
Mardis E., Menezes S.,
                Euteleostomi;
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CO1B_HUMAN
Q9BR76;
                                                                                         YQC2_CAEEL
Q09261;
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Matches
                                                               RESULT 9
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FEBS LECT. 244:34-38[1989].

FEBS LECT. 244:34-38[1989].

FEBS LECT. 244:34-38[1989].

FEBS LECT. 244:34-38[1989].

FRABILITY AND INHIBITS TRANSCRIPTION. IT ALSO BINDS TO SS-DNA AND RNA BUT WITH A WUCH LOWER AFFINITY. H-NS HAS POSSIBLE HISTONE-LIKE FUNCTION. MAX BE A GLOBAL TRANSCRIPTIONAL REGULANOR THROUGH ITS ABILITY TO BIND TO CUNFED DNA SEQUENCES, WHICH ARE FOUND IN REGIONS UPSTREAM OF A CERTAIN SUBSET OF PROMOTERS. IT PLAYS A ROLE IN THE THERMAL CONTROL OF PILI PRODUCTION. IT IS SUBJECT TO TRANSCRIPTIONAL AUTO-REPRESSION. IT BINDS PREFERRNIALLY TO THE UPSTREAM REGION OF ITS OWN GENE RECOGNIZING TWO SEGMENTS OF DNA ON BUTH. SIGNIANTS OF DNA ON BUTH. SIGNIANTS OF DNA ON BETTELLY TO THE UPSTREAM REGION OF ITS OWN GENE RECOGNIZING TWO SEGMENTS OF DNA ON BUTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-89171270; PubMed-2494066; La Teana A., Falconi M., Scarlato V., Lammi M., Pon C.L.; "Characterization of the structural genes for the DNA-binding protein
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                        Fernandes J.M.O., Smith v.J.;
"A novel antimicrobial function for a ribosomal peptide from skin secretions of rainbow trout.";
Submitted (APR-2002) to the SWISS-PROT data bank.
-i- FUNCTION: Has antibacterial activity against Gram-positive
                                                                                                                                                             -1- MASS SPECTROMETRY: MW-6676.6; METHOD-MALDI.
-1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
Ribosomal protein; Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE HISTONE-LIKE PROTEIN H-NS FAMILY.
PIR; S02776; S02776.
HSSP; P08936; 1HNR.
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Protacanthopteryg11; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_raxID=8022;
                                                                                                                                                                                                                                               18.6%; Score 11; DB 1; Length 11; 100.0%; Pred. No. 3.4e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
DNA-binding protein H-NS (Histone-like protein HLP-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AA; 15134 MW; B92C49F7995C5ED5 CRC64;
                                                                                                                                                                                                       NON_TER 11 11
SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Transcription regulation; Repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%; Score 7; DB 1;
100.0%; Pred. No. 3.3;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           133 AA
                                                 FUNCTION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001801; Histone_HNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00816; Histone_HNS; 1.
ProDom; PD007337; Histone_HNS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 16, Created)
                                                                                                                                                                                                                                                18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00528; HNS; 1
                                                                                                                                                                                                                                                                                                         1 KVHGSLARAGK 11
                                                                                                                                                                                                                                                                                                                         1 KVHGSLARAGK 11
                                                                                                                                                                                                                                                              Best Local Similarity
                                                              TISSUE-Skin mucus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=585;
                                                                                                                                                   bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990
01-NOV-1990
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNS OR HNSA
                                                                                                                                                                                                                                                                                                                                                                                                         HNS_PROVU
P18818;
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SEQUENCE
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                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                              Matches
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28 KTGRAKR 34

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                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - FUNCTION: MAY BE INVOLVED IN CYTOKINESIS, MOTILITY, AND SIGNAL TRANSDUCTION (BY SIMILARITY).
-i - SUBUNIT: BINDS ACTIN (BY SIMILARITY).
-i - SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
-i - SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas K.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 39.2 kba protein C32A3.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 346 AA; 39221 MW; D511225F5062B420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; Score 7; DB 1
100.0%; Pred. No. 7.5
:ive 0; Mismatches
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15-JUN 2002 (Rel. 41, Last sequ
15-JUN 2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 248241; CAA88285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WormPep; C32A3.2; CE01506.
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nes 7; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                           (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MECLINE-93187617; PubMed-8445371; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.; Molecular evidence that epizootic Venezular equine encephalitis (VEE) 1-AB viruses are not evolutionary derivatives of enzootic VEE subtype I-E or II viruses...; J. Gen. Virol. 74:519-523(1993).

I. FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.

I. FUNCTION: THE CAPSID PROTEIN CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

I. MISCELLANBOUG: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLS_EEVVM STANDARD; PRT; 1254 AA.
POLS_EEVVM STANDARD; 066589; 066590; 066591;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5Kructural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
6 kDa peptide; Spike glycoprotein E1].
Venezuelan equine encephalitis virus (strain Mena II).
Viruses; SSRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                  Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLED COIL (POTENTIAL).
A6012FDA683ECB59 CRC64;
                                                                                                                                                Genew; HGNC:2253; COROIB.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD400; 3.
ProDom; PD000018; WD40; 1.
SWART; SM00320; WD40; 3.
PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_2; 2.
ACLID-binding; Repeat; WD repeat; Coiled coil.
modified and this statement is not removed. entities requires a license agreement (See For Send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 7; DB 1
100.0%; Pred. No. 10;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , AAA42989.1; ALT_TERM.
; AAA42991.1; ALT_SEQ.
; AAA42992.1; ALT_SEQ.
; AAA42993.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WD 1.
WD 2.
WD 3.
WD 4.
                                                                                                                       EMBL; BC006449; AAH06449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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L04599;
L04599;
L04599;
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POLS_EEVVM
POLS_EEVVM
DT 01-JUN-
DT 01-JUN-
DE (Capsito)
CX 10-CUN-
DE (Capsito)
CX VEDRACE
CX NCBL_TR
RR SCOUEN
RX MEDLINI
RR SCOUEN
RT (VEE)
RT 
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                            Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase; Serine protease.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                        Length 1254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FBB-1996 (Rel. 32, Last annotation update)
40S xibosomal protein $27a.
Dictyostelium discoideum (Slime mold).
Eukaryota: Mycetozoa; Dictyostelium.
                                                                                                                                                                                              SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 KDA PEPTIDE.
SPIKE GLYCOPROTEIN E1.
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                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
. 22;
                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                         InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR001836; Alpha_core.
InterPro; IPR000930; Togavirin.
Pfam; PF00943; Alpha_E2_glycop; 1.
Pfam; PF01563; Alpha_core; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
Pfam; PF01569; Alpha_E3_glycop; 1.
                                                                                                                                                                                                                                                                                    POTENTIAL. POTENTIAL.
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N-LINKED
N-LINKED
N-LINKED
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EMBL; L04599; AAA42994.1; ALT_INIT.
PIR; JQ1979; JQ1979.
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100.08; Pic
0; }
                                                                                                                                                                                                                                                                                                                                                                 138343 MW;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                       P03315; 1VCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 24 KKKKKTG 30
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ACT_SITE
ACT_SITE
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TRANSMEM
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R27A_DICDI
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Nature 390:249-256(1997).
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EX7S_VIBCH
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          SO DE REPRESENTATION DE REPRES
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A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Bourise R., Bourshi C.V., Caldwell B., Capuano V., Carter N.M.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V. Carter N.M.,

RA Brouillet S., Devine K.M., Dusterholft A., Erlich S.D., Emmerson P.T.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Guiseppi G., Guy B.J., Haga K., Haiceh E., Foulger D.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kurita K., Lapidus A., Lardinois S., Haiceh J., Harwood C.R., Henaut A.,

A Cobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Presecan E., Pujic P., Purnelle B., Rosel B., Park S.H.,

RA Presecan E., Scallan E., Schleich S., Schroeter R., Scallan E., Schleich S., Schroeter R., Seron E., Pujic P., Purnelle B., Rose M., Sadaie Y.,

RA Tosaco V., Uchiyama S., Vandenbol M., Vannier R., Yasamoto K., Yata K.,

Minters P., Walder E., Wedler E.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogasawara N., Nakal S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                    Figure Francis American State State State (Figure Basic).

1 24 LYS-RICH (HIGHLY BASIC).
                                                                                                                                                                                                                                                                           F77B3E09D1B7246F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein S18 (BS21).
                                                                                                                                                                                                                                                                                                                                            Score 6; DB 1;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                              IPR002906; Ribosomal_S27.
1599; Ribosomal_S27; 1.
EMBL; M23750; AAA33264.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96051385; PubMed-7584024;
                                                                                                                                  Pfam; PF01599; R1bosomal_S27;
                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                   ZN_FING 46 69
SEQUENCE 78 AA; 8915 MW;
                                                                                                                                                                                                                                                                                                                                            10.2%;
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 1:1-14(1994).
                                PIR; E34080; UQDOR7
D1ctyDb; DD01026; -
InterPro; IPR002906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 KKKKKT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KKKKKT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RS18_BACSU
P21475;
                                                                                                                                                                                                                                                                                                                                            Query Match
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ID R318_BACSU
R718_BACSU
R718_BACSU
DT 01-MAY.
DT 01-MAY.
DT 01-MAY.
DT 10-MAY.
DE 30S r118
GN RPSIN.
GN RPSIN.
GN RPSIN.
GN NGBILIN
RR SCOUEN
RR MEDLINI

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STTER
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STRAIN=El TOR N16961, Serotype Ol;

MEDLINE=2040683; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Endlacya M.D., Vamathevan J., Bass S., Qin H., Brichardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
SEQUENCE OF 1-23.

MEDLINE-8219212; PubMed-6806564;

Higo K.I., Otaka E., Osawa S.;

"Purification and characterization of 30S ribosomal proteins from Bacillus subtilis: correlation to Escherichia coli 30S proteins.";

Mol. Genet. 185:339-244(1982).

-I FUNCTION: This protein has been implicated in aminoacyl-transfer.

-I FUNCTION: This protein has been implicated in aminoacyl-transfer.

-I FUNCTION: This protein has been implicated in aminoacyl-transfer.

-I FUNCTION: This protein has been implicated in aminoacyl-transfer.

-I FUNCTION: This protein has been implicated in aminoacyl-transfer.

-I FUNCTION: This protein has been implicated in aminoacyl-transfer.

-I FUNCTION: This protein has been implicated in aminoacyl-transfer.

-I FUNCTION: This PROTEINS.
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-!- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE
-ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable exodeoxylibonuclease VII small subunit (EC 3.1.11.6)
(Exonuclease VII small subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 AA; 8838 MW; 1CF19CE039C64FF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01084; Ribosomal_S18; 1.
PRINTS; PR00974; RIBOSOMALS18.
TODOm; PD002239; Ribosomal_S18; 1.
TIGRFAMS; TIGROOU165; S18; 1.
PROSITE; PS00057; RIBOSOMAL_S18; 1.
Ribosomal protein; RNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 6;
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EMBL; Z99124; CAB16126.1; ALT_INIT.
PIN; S11368; S11368.
Subtlinst; BG10047; rpsR.
InterPro; IPR001648; Ribosomal_S18.
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Matches 6; Conserv
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SEQUENCE
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11 SLARAG 16

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SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).

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NON_TER
SEQUENCE
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                                                           RESULT 16
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
             -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in grm 3/region (Fragment).
Micromonospora echinospora (Micromonospora purpurea).
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridee;
Actinomycetales; Micromonosporineae; Micromonosporacee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91192615; PubMed-2013410;
Kelemen G.H., Cundliffe E., Financsek I.;
"Cloning and characterization of gentamicin-resistance genes from
                                                                                                                                                                                                                                                                                                                                                                                      ;
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0
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                                                                                                                                                                                                                                                                                                                                                       Length 80;
                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AA; 11111 MW; 0B398039381DB012 CRC64;
                                                                                                                                                                                                                                                                            Pfam; PF02609; Exonuc_VII_S; 1.
TIGRFAMs; TIGR01280; xseB; 1.
Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE 80 AA; 8911 MW; F9B7F5A9C6821DD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micromonospora purpurea and Micromonospora rosea.", Gene 98:53-60(1991).
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100.0%; Pred. No. 28;
ive 0; Mismatches
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100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                  nterPro; IPR003761; Exonuc_VII_S.
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                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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Best Local Similarity
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Best Local Similarity
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                                                          SIMILARITY).
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44 SLARAG 49
                                                                                                                                                                                                                                                       VC0891;
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YGRM_MICEC
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5 SLARAG 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Micromonosporineae; Micromonosporaceae;
                                                                                                                                                                                                                                                                                                Kelemen G.H., Cundliffe E., Financsek T.;
Cloning and characterization of gentamicin-resistance genes from
Micromonospora purpurea and Micromonospora rosea.";
Gene 98:53-60(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
                                                             01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in GRM 3'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 6; DB 1;
100.0%; Pred. No. 28;
tive 0; Mismatches
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Last annotation update)
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105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 AA
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MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                                MEDLINE=91192615; PubMed=2013410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 37, Created)
(Rel. 37, Last sequ
(Rel. 40, Last anno
                                             (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M55521; AAA25339.1; -. PIR; PW0018; PW0018.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
    STANDARD;
                                                                                                                                Micromonospora rosea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=1878;
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                                                                                                                                                                                             Micromonospora
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50S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spirochete.";
                                         01-MAR-1992 (
01-FEB-1996 (
16-OCT-2001 (
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Strausberg R
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81 GSLARA
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EMBL;
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Science 281:375-388(1998).
-I- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SUBUNIT INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION OF THE AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92084127; PubMed-1748303;
L1 M., Latcud C., Center M.S.;
"Cloning and sequencing a cDNA encoding human ribosomal protein S25.";
Gene 107:339-333(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606, 10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21864036; PubMed-11875025;
Yoshihama M., Uechi T., Asakawa S., Kawasaki K., Kato S., Higa Maeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.;
"The human ribosomal protein genes: sequencing and comparative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 6; DB 1; Length 123;
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                                                                                                                                                                                                                                                                                                                  TIGR; TP0909; -.
InterPro; IPR01857; Ribosomal_L19.
InterPro; IPR0061857; Ribosomal_L19; 1.
PRINTS; PR00061; RIBOSOMALL19; 1.
ProDom; PD002979; Ribosomal_L19; 1.
PTGREAMS; TIGR01034; Fp1S_bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
RIBOSOMAL_L19; 1.
RIBOSOMAL E19; AM; 123E652CB4B545EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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SPECIES*Mouse; STRAIN*C57BL/6J;
                                                                                                                                                                                                                                                                                                  EMBL; AE001259; AAC65861.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysis of 73 genes.";
Genome Res. 12:379-390(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40s ribosomal protein S25.
RPS25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aarawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobor I., Basukawa T., Saito R., Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redischmann W., Gassterland T., Gissi C., King B., Kochlua H., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuki R., Tomita M., Gariboldi M., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchioni L., Mashima J., Mazamarelli N., Rodriguez I., Sakamato N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hayashizaki Y.;

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Will M., Mataka M., Kawaji H., Kohtsuki S., Matamarella M., Matamarella M., Mataka M., Kawaji H., Kohtsuki S., Matamarella M., Matamarella M., Matamarella M., Matamarella M., Matamarella M., Kawaji H., Kohtsuki S., Matamarella M., Matamarella M., Kawaji H., Kohtsuki S., Matamarella M., Matamarella M., Kawaji H., Kohtsuki S., Matamarella M., Matamare
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Biochem. Biophys. Res. Commun. 186:1688-1693(1992).
-!- SIMILARITY: BELONGS TO THE S25E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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MEDLINE-92378645; PubMed-1354961;
Chan Y.-L., Wool I.G.;
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100.0%; Pred. No. 33;
ive 0; Mismatches
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InterPro; IPR004977; Ribosomal_S25.
Pfam; PF03297; Ribosomal_S25; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             Nature 396:133'140(1998).

-I'- FUNCTION: S11 PLAYS AN ESSENTIAL ROLE FOR THE SELECTION OF THE CORRECT TRNA IN PROTEIN BIOSYNTHESIS. IT IS LOCATED ON THE LARGE LOBE OF THE SMALL SUBDINIT (BY SIMILARITY).

-I'- SIMILARITY: BELONGS TO THE S11P FAMILY OF RIBOSOMAL PROTEINS.
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NCBI_TaxID=6239;
                                                                                                                                                                                                                               MEDLINE-99939499; PubMed-9823893; Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Pondowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Rickettsleae; Rickettsia.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 13.7 kDa protein C18H9.2 in chromosome II.
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        127 AA
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InterPro; IPR001971; Ribosomal_S11.
Probom; PD00411; Ribosomal_S11.1
Probom; PD001010; Ribosomal_S11; 1.
PROSITE; PS00054; RIBOSOMAL_S11; FALSE_NEG.
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100.0%; Pred. No. 33;
iive 0; Mismatches
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                                       Created)
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SEQUENCE 127 AA; 13583 MF
                                30-MAY-2000 (Rel. 39, Creat 30-MAY-2000 (Rel. 39, Last 16-ccr-2001 (Rel. 40, Last 30S ribosomal protein S11. RPSK OR RF636.
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                    Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKKKKT 13
                                                                                                                                                                                                                                                                                                                   mitochondria.
   RS11_RICPR
Q9ZCS8;
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Q09237;
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YQ82_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@issenit(See http://www.isb-sib.ch/announce/or send an email to license@issenic.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mallet L., Bussereau F., Jacquet M.;
A4 3.5 Kb segment of yeast chromosome XIV, which contains MFA2,
MFP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetes;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical 15.3 kDa protein in MFA2-MEP2 intergenic region.
YNL143C OR N1206 OR N1795.
Saccharomyces cerevistae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetisetales; Saccharomycetaceae; Saccharomycet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
Protein in IXRI-TFA1 intergenic region.
                                                                                                                                                                                                 0; Indels
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                                                                          EMBL; U23147; AAC46687.1; -. WormPep; C18H9.2; CE01802. Hypothetical protein. SEQUENCE 128 AA; 13666 MW; C7A64D960B95E2EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 246843; CAA86883.1; -.
EMBL; 271419; CAA96026.1; -.
SGD; S0005087; YNL143C.
Hypothetical protein: SEQUENCE 130 AA; 15319 MW; 29070E47FC63436D CRC64;
                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 6; DB 1;
100.0%; Pred. No. 34;
tive 0; Mismatches
                                                                                                                                                       10.2%; Score b; 23.100.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                           130 AA.
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                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96109932; PubMed=8619318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
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(Rel. 29, I
(Rel. 32, I
1 15.6 kDa F
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Best Local Similarity
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84 KKKKKT
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P36098;
01-JUN-1994 (
01-JUN-1994 (
01-NOV-1995 (
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P53908;
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ID YKDI_XI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (RPS16A).
STRAIN-S28BC / AB972;
Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RS16_VEAST STANDARD; PRT; 142 AA.
P40213; P26787;
01-A0G-1992 (Rel. 23, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
40S ribosomal protein S16 (RP61R).
(RPS16A OR RP61R OR YMR143W OR YM9375.12) AND (RPS16B OR YDL083C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92184799; Pubmed-1544921;
Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
"NH2-terminal acetylation of ribosomal proteins of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 267:5442-5445(1992).
-!- MISCELLANEOUS: THERE ARE TWO GENES FOR S16 IN YEAST.
-!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                             Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (RPS16B).
Wambutt R., Wedler H., Wedler E., Scharfe M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              142 AA; 15739 MW; 19408A7791FF4356 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15873374B3262144 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00380; Ribosomal_S9; 1.
Probom; PD001627; Ribosomal_S9; 1.
PROSTITE; PS00360; RIBOSOMAL_S9; 1.
Ribosomal protein; Acetylation; Multigene family.
                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                          100.0%; Pred. w.
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                                                                                                                                                                                             Score 6; I
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 247071; CAA87357.1; -.
EMBL; 274131; CAA98649.1; -.
EMBL; 20004751; RPS16A.
SGD; S0002241; RPS16B.
InterPro; IPR000754; Ribosomal_S9.
                 InterPro: IPR000754; Ribosomal_S9.
Pfam; PF00380; Ribosomal_S9, 1.
ProDom; PD001627; Ribosomal_S9; 1.
PROSITE; PS00360; RIBOSOMAL_S9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 AA; 15716 MW;
    EMBL; AL033497; CAA21965.1;
                                                                                                                                                                                             10.2%;
                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                  Ribosomal protein.
                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                          48 TFGKKK 53
                                                                                                                                                                                                                                                                                                                        | | | | | | | | | | 8 TFGKKK 13
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RS16_YEAST
                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                            Purnelle B., Skala J., van Dyck L., Goffeau A.;
"Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new tRNA gene and four new open reading frames including a leucine zipper proctein and a homologue to the yeast mitochondrial regulator ABF2.";
Peast 10:125-130(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
82908E65C7E37CFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT subcommal protein S16.
RPS16 OR CA49C10.01C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 AA
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100.0%; Pred. No. 35;
tive 0; Mismatches
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EMBL; Z28031; CAA81866.1; -.
PIR; S37848; S37848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                      MEDLINE-94262309; PubMed-8203146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 129 PC
137 AA; 15626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0001514; YKL031W. Hypothetical protein; TTRANSMEM 36 52
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YKL031W OR YKL244.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                              NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5476;
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094017;
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TO RS16_C
TO O94017
DT 16-OCT
DT 16-OCT
DE 40S r1
DE 40S r1
DE A0S CANAL
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RP SEQUEN
RP 
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NCBI_TaxID=4932;
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RPL14 OR LPD23.
 AGKVRG 14
                    AGKVRG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 EKKKKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RL14_LEIDO
Q25278;
                                                                           YK20_YEAST
P36133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=LS;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                KK20_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RL14_LEIDO
σ
                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 27
                                                      RESULT
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the ENBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                   "Nucleotide sequence and primary structures of gene products coded for by the T4 genome between map positions 48.266 kb and 39.166 kb."; Nucleic Acids Res. 15:3632-3633(1987).
                                                                                                                                                                                                                                                                                                        MEDLINE-89065345; PubMed-2974005; Barth K.A., Powell D., Trupin M., Mosig G.; Regulation of two nested proteins from gene 49 (recombination endonuclease VII) and of a lambda RexA-like protein of bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan; PF02945; endonuclease_7; 3.
Hydrolase; Endonuclease; Nuclease; Alternative initiation.
CHAIN 1 157
RECOMBINATION ENDONUCLEASE VII, LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- ALTERNATIVE PRODUCTS: 2 isoforms are produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage T4.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECOMBINATION ENDONUCLEASE VII,
                                                                       END7_BPT4 STANDARD; PRT; 157 AA.
P13340; Q38426; Q9T0V4;
P1340-1390 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Recombination endonuclease VII (EC 3.1.-.-) (Protein GP49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOR SHORT ISOFORM,
86233D2A7FC0F9A8 CRC64;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE INITIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.0%; Pred. No. 40; 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y00122; CAA68307.1; -.
EMBL; AF158101; AAD42477.1; -.
EMBL; AF158101; AAD42687.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR004211; Endonuclease_7.
                                                                                                                                                                                                                            MEDLINE-87203398; PubMed-3575111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 F
18144 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X12629; CAA31148.1; -. EMBL; X12629; CAA31149.1; -.
                                                                                                                                                                                                                                          Comaschewski J., Rueger W.;
                                                                                                                                                                                                                                                                                                                                                              Genetics 120:329-343(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HETERODUPLEX LOOPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A30291; ZNBPT9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
48 TFGKKK 53
                     8 TFGKKK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                     RESULT 25
                                                                END7_BPT4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campos-Neto A., Soong L., Cordova J.L., Sant'Angelo D., Skeiky Y.A.W., Ruddle N.H., Reed S.G., Janeway C. Jr., McMahon-Pratt D.; Red S.G., Janeway C. Jr., McMahon-Pratt D.; Red S.G. a Leishmania donovani gene instructed by a peptide isolated from major histocompatibility complex class II molecules of infected macrophages."; J. Exp. Med. 182:1423-1431(1995).

- SIMILARITY: BELONGS TO THE LIJE FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leishmania donovani.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable 40S ribosomal protein L14 (23 kDa cell surface protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                             Last sequence update)
Last annotation update)
protein in GAP1-NAP1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Urrestarazu L.A., Jauniaux J.-C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYS-RICH (HIGHLY BASIC).
51BC98B657A720C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 6; DB 1
100.0%; Pred. No. 42;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96042140; PubMed-7595213;
                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
15-DEC-1998 (Rel. 37, Last ann
Hypothetical 19.2 kDa protein i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 167 L
167 AA; 19222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 228265; CAA82114.1; -. EMBL; 228266; CAA82117.1; -. PIR; S38112; S38112. SGD; SO001748; YKR040C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein
DOMAIN 144 16
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaawa K., Izawa M., Nishi K., Kiyosawa H., Koaukawa T., Saito R., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Reischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Androne D., Boffelli D., Bojunga N., Carninci P., de Bonaldd M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamico N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wishbar-Boolis A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshar-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
FXVD domain-containing ion transport regulator 5 precursor (Oncoprotein-Induced protein 2) (Ion channel homolog RIC) (EF-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fu X., Kamps M.P.;
"E2a-Pbx1 induces aberrant expression of tissue-specific a
developmentally regulated genes when expressed in NIH 3T3
                                                                                                                                                                                                                                                                                                                                                                                        Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                           175 AA; 19887 MW; A3F9AFF30D986814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                        10.2%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AA.
                                                                                                                                                                                                  EMBL; X86551; CAA60246.1; -.
InterPro; IPR000302; KOW_motif.
InterPro; IPR002784; Ribosomal_L14e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell. Biol. 17:1503-1512(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE-Spleen;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                      Pfam; PF00467; KOW; 1.
Pfam; PF01929; Ribosomal_L14e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97184476; PubMed-9032278;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (Mouse)
                                                                                                                                                                                                                                                                                                                      Ribosomal protein. SEQUENCE 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 AKRRMQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 AKRRMQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXYDS OR OIT2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FXYS_MOUSE
P97808;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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1D FXYS_MOUSE

1D FYSO_M

DT 15-JUL

DT 15-JUL

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DT 15-JUL

DE (ONCO PRICE

RN HISTAIN

RN HELLIN

RN ALSAWA

RN SSILO

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RN SCHLIM

RN GLOIN

RN GRACH

RN GLOIN

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00000000008888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93293845; PubMed-8514766;
Chen W., Lim H., Lim L.;
"The CDC42 homologue from Caenorhabditis elegans. Complementation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: HIGHEST LEVELS AT THE EMBRYONIC STAGE, DECREASING PROGRESSIVELY DURING DEVELOPMENT, EXCEPT FOR AN INCREASE AT THE L3 STAGE.
SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
-i- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-i- TISSUE SPECIFICITY: SPLEEN, LUNG, SKELETAL MUSCLE, AND TESTIS.
-i- DEVELOPMENTAL STAGE: EXHIBITS BIPHASIC EXPRESSION DURING
                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. FXYD DOMAIN-CONTAINING ION TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 6; DB 1; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466FBF1E05D861C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       !ransmembrane; Signal; Ionic channel; Ion transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cell division control protein 42 homolog (CDC42CE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AA
                                                                      SIMILARITY: BELONGS TO THE FXYD FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATOR 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO-RICH.
                                                                                                                                                                                                                                                                                         MGD; MGI:1201785; FXYd5.
InterPro; IPR000272; ATP101_PLM_MAT8.
PFfam; PF00138; ATP1G1_PLM_MAT8; 1.
PROSITE; PS01310; FXYD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yeast mutation.";
J. Biol. Chem. 268:13280-13285(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Sc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 PI
19454 MW;
                                                                                                                                                                                                                                                      EMBL; U72680; AAB51040.1; -. EMBL; AK003068; BAB22545.1; -
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178
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166
178
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146
167
188
178 AA;
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les 6; Conserv
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                                                       DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 RGQTPK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIIIII
RGQTPK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
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Q05062;
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SEQUENCE
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TRANSMEM
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GYPASE-ACTIVATIOR PROTEIN (GAP).

SIMILABITY: BELONGS TO THE SMALL GYPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: RAS PROTEINS BIND GDP/GTP AND POSSESS INTRINSIC GTPASE
                                                                                                                                                                                                                                                                                                             GTP-binding; Lipoprotein; Cell cycle; Cell division; Prenylation. NP_BIND 7 14 GTP (BY SIMILARITY). NP_BIND 54 58 GTP (BY SIMILARITY). NP_BIND 112 115 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Spleen;
MEDLINE=97080492; PubMed=8921837;
Chajut A., Gazit A., Yaniv A.;
"The turkey c-raplA proto-oncogene is expressed via two distinct promoters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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GERANYL-GERANYL (BY SIMILARITY).
8733958968681299 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 188;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transforming protein p21 (K-Ras) (Ki-Ras).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 46;
0; Mismatches
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                                                                                                                                                                      WormPep; R07G3.1; CE02020.
InterPro: IPR001378; GTPase_Rho.
InterPro: IPR001806; Ras_trnsfrmng.
InterPro: IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                     EMBL; L10078; AAA51433.1; -.
EMBL; U23452; AAK31543.1; ALT_INIT.
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SMART; SM00174; RHO; 1.
TIGRFAMS; TIGRR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    20823 MW;
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Conservative 0
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                                                                                                                                        PIR; A46578; A46578.
HSSP; P21181; 1AM4.
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Gene 177:7-10(1996).
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P79800;
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Baga M., Norgren M., Normark S.; "Biogenesis of E. coli Pap pili: papH, a minor pilin subunit involved in cell anchoring and length modulation."; cell 49:241-251(1987).
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"Nucleotide sequence, regulation and functional analysis of the pape gene regulated for cell surface localization of Pap pili of uropathogenic Escherichia coli.";
Mol. Microbiol. 1:169-178(1987).
-!- FUNCTION: FTHBRIAR (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELLUM OF SPECIFIC HOST ORGANS.
-!- FUNCTION: PAPH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL. IN ADDITION THE STOLGHLOMETRIC RELATIONSHIP BETWEEN PAPH AND PAPA DETERMINES THE PILUS LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93023852; PubMed-1357526; Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M., Lindberg F., Gaastra W., Normark S., "Horizontal gene transfer of the Escherichia coli pap and prs pill operons as a mechanism for the development of tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                     GPP-binding; Prenylation; Lipoprotein.

The GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

A 40 EFFECTOR REGION (BY SIMILARITY).

FRINESYL (BY SIMILARITY).

AA: 21452 MW; AAB6C319BB259B65 CRC64;
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15-DEC-1998 (Rel. 37, Last annotation update)
PAP fimbrial minor pilin protein precursor.
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HSSP; P01112; 1PLL.
InterPro; IPR001577; GTPase_Ras.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRIWYS; PR00449; RASTRNSFRMG.
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                                                                                                                         TIGRFAMS; TIGR00231; small_GTP; 1.
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01-APR-1988 (Rel. 07, Last sequ
15-DEC-1998 (Rel. 37, Last anno
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SEQUENCE OF 149-195 FROM N.A.
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SEQUENCE FROM N.A.
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116
32
185
                                                                                                                                        Proto-oncogene;
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P07111;
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                                                                           ; ORGANISM: Homo sapiens US-09-925-299-1098
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US-09-764-869-926
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                       Best Loc
Matches
                                                                                                 NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1098
LENGTH: 48
TYPE: PRT
                                                Query Match
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - NUMBER OF SEQ ID NOS: 2442 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
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OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (40)
                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                           FILE REFERENCE: PA102
                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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NAME/KEY: SITE
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24 KKKKKT 29
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                       Similarity 6; Conserv
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                       Score 6; DB 1; Pred. No. 27; 0; Mismatches
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Pred. No.
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PRIOR APPLICATION NUMBER: EARLIER
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Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
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Best Local (
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SEQ ID NO 1820
LENGTH: 36
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CURRENT FILING DATE: 2001-01-17
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TYPE: PRT
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LOCATION: (35)
OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                              NAME/KEY: SITE LOCATION: (36)
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SEQ ID NO 1633
LENGTH: 43
TYPE: PRT
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                                             NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: X
NAME/KEY: SITE
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
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OTHER INFORMATION:
NAME/KEY: SITE
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ORGANISM: Homo sapiens
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids {\tt US-09-925-299-1319}
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                                                                                                                           ; MOLECULE TYPE: US-09-071-838-189
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Best Local S
Matches 6
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Patent No
                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                      TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: :
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OTHER INFORMATION:
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                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//09/071,838
FILING DATE: 01-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
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                             TFGKKK 53
TFGKKK 6
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. US20020152501A1
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Yadegari, Ramin
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                                                            Conservative
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                                                                          10.2%; Score 6; 100.0%; Pred. No.
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US-09-764-846-248
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PRIOR EILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1474
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
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LENGTH: 31
TYPE: PRT
ORGANISM: Homo sapiens
                                                                              Query Match
Best Local Similarity
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                                                                Matches
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CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 348 SOFTWARE: Patentin Ver. 2.0
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NAME/KEY: SITE
LOCATION: (31)
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TYPE: PRT
                                                                                                                                                                 OTHER INFORMATION:
NAME/KEY: SITE
LOCATION: (31)
                                                                                                                                                                                                                  NAME/KEY: SITE
LOCATION: (30)
                                                                                                                                                                                                                                                   LOCATION: (25)
OTHER INFORMATION:
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NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
17
                             23 EKKKKK 28
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es 6; Conserv
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EKKKKK 22
                                                               Conservative
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100.0%; Pred. No. 19
:ive 0; Mismatches
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Pred. No.
                                                                Mismatches
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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: ACCOMPACA **.1
CURRENT APPLICATION NUMBER: U$/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: U$ 60/180,312
PRIOR APPLICATION NUMBER: U$ 60/207,456
PRIOR APPLICATION NUMBER: U$ 09/632,366
PRIOR APPLICATION NUMBER: U$ 60/236,359
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Best Local Similarity 100.
George Conservative
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
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APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
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100.0%; Pred. No.
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%; Pred. No. 11;
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1319
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US-09-925-299-1319
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Best Local
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                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US00/05883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 49117
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
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OR APPLICATION NUMBER: PCT/US01/00662
OR APPLICATION NUMBER: PCT/US01/00661
OR APPLICATION NUMBER: PCT/US01/00661
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00670
OR APPLICATION NUMBER: PCT/US01/00670
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7

N: EXPRESSED IN BARIN, SIGNAL = 2.7

N: EXPRESSED IN BONE MARROW, SIGNAL = 5.6

N: EXPRESSED IN LUNG, SIGNAL = 5.7

N: EXPRESSED IN HELA, SIGNAL = 3.6

N: EXPRESSED IN HEART, SIGNAL = 3.6

N: EXPRESSED IN HEART, SIGNAL = 4.8
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100.0%; Pr
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; Pred. No. 16
0; Mismatches
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NAME/KEY: SITE LOCATION: (17)

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US-09-945-249-87
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Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
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SEQ ID NO 87
LENGTH: 15
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PRIOR APPLICATION NUMBER: 09/041,990
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: 08/771,212
PRIOR FILING DATE: 1996-12-20
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PRIOR FILING DATE: 1996-04-11
NUMBER OF SEQ ID NOS: 89
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                                                                                                APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
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INVENTION: No. US20020164786Alel Telomerase
F SEQUENCES: 225
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Pred. No. 11;
0; Mismatches
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US-09-438-486-201
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
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APPLICATION NUMBER:
FILING DATE: 18-APR-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
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APPLICANT:
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CITY: San Francisco
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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mes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94111-3834
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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VENTION: No. US20030009019Alel Telomerase
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18-APR-1997
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.30
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                                                                                                                                              US 08/724,643
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5. 11;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 155
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-774-639-155
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US-09-74-639-155
Sequence 155, Application US/09774639
Publication No. US200300035581
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PZ013P1
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US-10-014-717-5
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US-09-764-877-1759
                                                                                                                                                                                                                                                  Sequence 5, Application US/10014717 Publication No. US20020192778A1 GENERAL INFORMATION:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
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Best Local S
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
                                                                                                                                  APPLICANT:
                                                                                                                                                                    APPLICANT: Schupp, Thomas APPLICANT: Ligon, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 10.0%; Score 7; 1 10.0%; Pred. No. 10.0%
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Cyr, Devon
Goerlach, Joern
                                                                                                                     Molnar, Istvan
                                                                                  Zirkle, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%; Score 7;
100.0%; Pred. No.
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o. 6.7;
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Best Local Similarity
Watches 7; Conserve
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; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-10-014-717-5
                                                                                      Sequence 87, Application US/09945249
Patent NO. US20020168748A1
GENERAL INFORMATION:
APPLICANT: BERLIN, VIVIAN
APPLICANT: DAMAGNEZ, VERONIQUE
APPLICANT: SMITH, SUSAN E.
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CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: UP 294795/2001
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: UP 227094/2001
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: UP 6910/2001
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: UP 401417/2000
PRIOR APPLICATION NUMBER: UP 401417/2000
PRIOR APPLICATION NUMBER: UP 401417/2000
PRIOR FILING DATE: 2000-12-28
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09983067 Patent No. US20020123101A1
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.2%; Score 6; Best Local Similarity 100.0%; Pred. No. Matches 6; Conservative 0; Mismatc
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                APPLICANT: DAMAGNEZ, VERONIQUE
APPLICANT: SMITH, SUSAN E.
TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
TITLE OF INVENTION: AND USES RELATED THERETO
FILE REFERENCE: MIV-074.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR FILING DATE: 199-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Process for Producing Peptides By Using In Vitro TITLE OF INVENTION: Transcription/Translation System FILE REFERENCE: 1752-0151P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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CURRENT FILING DATE: 2001-11-13
FILE REFERENCE: MIV-074.06
CURRENT APPLICATION NUMBER: US/09/945,249
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TYPE: PRT
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UEDA, Takuya
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b. 1.7e+02
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Hanzel, David I Chen, Wensheng

David K.

FOR

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; OTHER INFORMATION: E
; OTHER INFORMATION: E
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; OTHER INFORMATION: E
US-09-864-761-35333
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                                                                                                                                                                                        Query Match
Best Local
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION:
OTHER INFORMATION:
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       56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 2001-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                               KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
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N: EXPRESSED IN BRAIN, SIGNAL = 5.5

N: EXPRESSED IN BONE MARROW, SIGNAL = 9.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1

N: EXPRESSED IN HEA74, SIGNAL = 12

N: EXPRESSED IN HEART, SIGNAL = 12

N: EXPRESSED IN HELA, SIGNAL = 12
                                                                                                                                                                                                                                                                                                                                                                1: MAP TO ACO09704.2
1: EXPRESSED IN LUNG,
1: EXPRESSED IN PLACEN
1: EXPRESSED IN PLACEN
1: EXPRESSED IN BRAIN,
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                                                                                                                                                                            Score 28;
Pred. No.
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ADULT LIVER, SIGNAL
                                                                                                                                                Mismatches
                                                                                                                                                                                DB 10;
2.8e-19;
                                                                                                                                                                                                               Length 118;
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-39484
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US-09-864-761-39484
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 39484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Annomax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica X-1 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                OTHER INFORMATION: MAP TO OTHER INFORMATION: EXPRESS OTHER INFORMATION: EXPRESS OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                            ORGANISM: HOMO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 7.1

N: EXPRESSED IN LUNG, SIGNAL = 7.4

N: EXPRESSED IN HELA, SIGNAL = 7.2

N: EXPRESSED IN HELA, SIGNAL = 7.2

N: EXPRESSED IN BEARIN, SIGNAL = 7.3

N: EXPRESSED IN BONE MARROW, SIGNAL = 6.2

N: EXPRESSED IN BONE MARROW, SIGNAL = 6.2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Listing Engine vers. 1.1
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2000-06-30
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Score 7; DB 1
3; Pred. No. 3.9
0; Mismatches
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                                           Length 62
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Matches

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Match Length
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13:
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        Published_Applications_AA: *
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: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
0: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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2: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US0_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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10 US-09-864-761-3533

10 US-09-764-877-1759

10 US-09-774-639-155

10 US-09-983-067-1

10 US-09-983-067-1

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10 US-09-864-676-201

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10 US-09-764-869-729

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Sequence 5, Appli
Sequence 87, Appli
Sequence 87, Appl
Sequence 201, App
Sequence 201, App
Sequence 729, App
Sequence 1197, Ap
Sequence 1189, App
Sequence 1184, App
Sequence 1144, App
Sequence 1143, Ap
Sequence 1143, Ap
Sequence 1140, Ap
                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                           Sequence 994, App
Sequence 35333, A
Sequence 39484, A
Sequence 1759, Ap
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Sequence 5, Appli
Sequence 1, Appli
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	05-09-704-840-242	115-00-764-846-242	US-09-925-300-1105	US-09-764-846-179	US-09-925-299-1340	US-09-764-846-191	US-09-201-936-19	US-09-201-936-18	US-09-867-550-284	US-09-764-877-1089	US-09-764-846-224	US-09-864-761-45501	US-09-764-846-260	US-10-117-604-2	US-09-925-301-1475	US-09-925-300-1198	US-09-989-919-118	US-09-864-761-47812	US-09-864-761-47593	US-09-764-847-601	US-09-764-855-113	US-09-764-869-1228	US-09-983-802-479	US-09-925-299-1098	US-09-764-869-926	us-09-925-301-1633
polyconoc // oppor	sequence 444, App	ا د	1105,	Sequence 179, App	Sequence 1340, Ap	Sequence 191, App	Sequence 19, Appl	Sequence 18, Appl	4, ,	1089,	Sequence 224, App	45501	Sequence 260, App	Sequence 2, Appli	Sequence 1475, Ap	Sequence 1198, Ap	Sequence 118, App	Sequence 47812, A	47593	Sequence 601, App	113,	e 1228	Sequence 479, App	Sequence 1098, Ap	9	Sequence 1633, Ap

ALIGNMENTS

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; SEQ ID NO 994
; LENGTH: 170
; TYPE: PRT
; ORCANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-994
: Sequence 35333, Application US/09864761
Patent NO. US20020048763A1
: GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
                                                                                                        RESULT 2
US-09-864-761-35333
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US-09-925-301-994
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;

FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 994, Application US/09925301
; Patent No. US20020052308A1
                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 59; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR ETILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                            1 KVHGSLARAGKVRGQTPKVAKQEKKKKXTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
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                                                                                                                                                                                                                                                                                Score 59; DB 10;
Pred. No. 9.3e-48;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        Length 170;
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SETTER

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RESULT 32
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ID PRSH_E
AC P42185
DT 01-NOV
DT 01-NOV
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Best Local
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                                                                                                     BÖHCESIVE PROPERTIES.";

MOI. MICROBIOI. 6:2225-2242(1992).

MOI. MICROBIOI. 6:2225-2242(1992).

PROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5

MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.

PROCTION: PRSH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL.
IN ADDITION THE STOICHTOMETRIC RELATIONSHIP BETWEEN PRSH AND PRSA DETERMINES THE PILUS LENGTH.

SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00529; CAA68587.1; -. EMBL; M16202; AAA24286.1; -. EMBL; X61239; CAA43563.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M.,
Lindberg F., Gaastra W., Normark S.;
"Horizontal gene transfer of the Escherichia coli pap and prs pili
operons as a mechanism for the development of tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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Pfam; PF00419; Fimbrial; 1.
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93023852; PubMed=1357526;
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URINARY TRACT PRODUCE PAP-PILI WHICH ARE HAIT-LIKE APPENDA
CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGALACTOSIDE-
ween the SW155 INSTITUTE. The European Bioinformatics Institute. The European Bioinformatics as long
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58
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. 32, Last sequ
. 37, Last anno
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195 P
97 P
21835 MW;
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37, Last annotation update)
pilin protein precursor.
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Pred. No. 48;
0; Mismatches
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Query Match

SEQUENCE

198 AA;

22541 MW;

67C262585D3BEA3A CRC64;

LYS/

/SER-RICH

10.28;

Score 6;

DB 1;

Length 198;

136

DOMAIN

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RMRP_YEAST
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Best Local S
Matches
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P40993;
                                                                                                                                                                                                                                                                           Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan
Hunicke-Smith S., Hyman R., Komp C., Lashkarl D., Lew H., Lin E
Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.
Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
Winant A., Yelton M., Botstein D., Davis R.W.;
Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: ESSENTIAL COMPONENT OF THE MRP RIBONUCLEOPROTEIN
ENDORIBONUCLEASE THAT CLEAVES MITOCHONDRIAL PRIMER RNA SEQU-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmitt M.E., Clayton D.A.; "Characterization of a unique protein component of yeast RNase MRP: an RNA-binding protein with a zinc-cluster domain."; Genes Dev. 8:2617-2628(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
RNase MRP protein component SNM1.
SNM1 OR YDR478W OR D8035.21.
SGD; S0002886; SNM1.
Hydrolase; Nuclease; RNA-binding.
                                       EMBL; Z37982; CAA86054.1;
EMBL; U33050; AAB64905.1;
PIR; S48236; S48236.
                                                                                                                     use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                            This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
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PRS FIMBRIAL MINOR
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Mismatches
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                                                                                                                                         http://www.isb-sib
                                                                                                                                                            Usage
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lung E., Duncan M.,
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RESULT 34
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                                                                                                                                     Genew; HGNC:7227; MRAS.
InterPro; IPR003577; GTPase_Ras.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001230; Ras_trnsfrmng.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfan; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00173; RAS; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
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30-MAY-2000
15-JUN-2002
                       NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98062166; PubMed=9400994; Kimmelnan A., Tolkacheva T., Lorenzi M.V., Osada M., Chan A.M.-L.; "Identification and characterization of R-ras3: a novel member of RAS gene family with a non-ubiquitous pattern of tissue distribution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99409042; PubMed=10477695;
Louahed J., Grasso L., de Smet C., van Roost E., Wilcolaides N.C., Levitt R.C., Renauld J.-C.;
"Interleukin-9-induced expression of M-Ras/R-Ras3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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                                                                                            NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Od 94:1701-1710(1999).

FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A REPURCTION: METAKLY IN CONTROLLING CELL PROLIFERATION. WEAKLY ACTIVATES THE MAP KINASE PATHWAY.

TISSUE SPECIFICITY: EXPRESSION HIGHLY RESTRICTED TO THE BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: BY INTERLEUKIN-9, BUT NOT BY IL-2 OR IL-4. SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
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P01112; 1F
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                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
;; Prenylation; 1
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71
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185 191
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
protein M-Ras (Ras-related protein R-Ras3).
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AAD02287.1; -.
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Catarrhini; Hominidae;
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PRINTS; SMART; S

SM00173;

RAS;

small_GTP;

RASTRNSFRMNG

Small_GTP Ras_trnsfrmng

InterPro; IPR005225;
Pfam; PF00071; ras;
PRINTS; PR00449; RAS

InterPro; InterPro; InterPro;

IPR001806;

IPR003577; GTPase_Ras.
IPR001230; Prenyl_site.

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RESULT TO COLUMN AND RESULT TO
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MRAS OR XRAS.
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008989;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leslie K.B., Schrader J.W.;

Leslie K.B., Schrader J.W.;

"Characterization of a transforming, novel ras-related molecule.",

"Characterization of a transforming, novel ras-related molecule.",

"Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

-i- FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NO

UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY

ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).

-i- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
                                                                                                                                                                        EMBL; AB004879; BAA20538.1;
EMBL; AF043581; AAD02277.1;
EMBL; AF031159; AAD01926.1;
HSSP; P01112; 1PLK.
MGD; MGI:1100856; Mras.
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SEQUENCE
                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99409042; PubMed-10477695;
Louahed J., Grasso L., de Smet C., van Roost E.,
Nicolaides N.C., Levitt R.C., Renauld J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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"Novel small GTPase M-Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=98055615; PubMed=9395237;
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16-OCT-2001
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1)1 (Rel. 40, Last sequence upd)
1) (Rel. 40, Last annotation upd)
2) protein M-Ras (Ras-related)
2) Ras (X-Ras).
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t annotation update)
(Ras-related protein R-Ras3) (Muscle and
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; 0B2B55AFA96B3EC4 CRC64;
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1. FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NUPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. MEAKLY ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).

1. TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE CELLS.

1. SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                       TIGREAMS; TIC
GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003577; GTPase_Ras.
InterPro; IPR001230; Prenyl_Site
InterPro; IPR001806; Ras_trnsfrn
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D89863; BAA20531.1; -. HSSP; P01112; 1PLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytoskeleton
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"Novel small GTPase M-Ras participates
cytoskeleton.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98055615; PubMed=9395237;
Matsumoto K., Asano T., Endo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene 15:2409-2417(1997).
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                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00071; ras;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISION TO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 KKKKKT 190
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resident ras; 1
resid
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                                                                                                                                                                                                                                                                                                                                           PRO0449; RASTRNSFRMNG.
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Pred. No
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; 975CFDD1FDF37FCF CRC64;
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RESULT 37
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Best Local 9
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ighp.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the endocellular bacterial symbiont of aphids buchnera sp. APS.";

Nature 407:81-86(2000).

-i- FUNCTION: RIBOFLAVIN SYNTHASE IS A BIFUNCTIONAL ENZYME COMPLETOR THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-CATALYZING THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Tokyo 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M
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REPEAT
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                                                                                                                                                                                                                     EMBL; AP001118; BAB12830.1; InterPro; IPR001783; Lum_binding. Pfam; PF00677; Lum_binding; 2. ProDom; PD004110; Lum_binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RISA_BUCAI
                                                                                                                                           Riboflavin biosynthesis; Transferase;
                                                                                                                                                                     TIGRFAMS; TIGRO0187; T1bE; 1. PROSITE; PS00693; LUM_BINDING;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIBITYL-AMINO-2,4(1H,3H)-PYRIMIDINEDIONE AND L-3,4-DIHYDROHY-2-BUTANONE-4-PHOSPHATE VIA 6,7-DIMETHYL-8-LUMAZINE. THE ALPHA SUBUNIT CATALYZES THE DISMUTATION OF 6,7-DIMETHYL-8-LUMAZINE TO RIBOFLAVIN AND 5-AMINO-6-(1'-D)-RIBITYL-AMINO-2,4(1H,3H)-PYRIMIDINEDIONE (BY SIMILARITY).

CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine riboflavuh + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

PATHMAY: FINAL STEPS OF RIBOFLAVIN SYMTHESIS.

SUBUNIT: OLIGOMER THAT CONSIST OF 3 ALPHA SUBUNITS AND 60 BETA SUBUNITS (BY SIMILARITY).

SUBUNITS (BY SIMILARITY).
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           23505
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endocellular bacterial symbiont of
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     BINDS TO LUMAZINE (PROBABLE)
BINDS TO LUMAZINE (PROBABLE)
; 7CCE3272CF54BA5B CRC64;
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                                                                                                                                        Complete proteome.
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Query Match Best Local (

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P06780;
01-JAN-1988
01-JAN-1988
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers A.M., Crivellone M.D., Tzagoloff A.;
"Assembly of the mitochondrial membrane system. MRP1 and MRP2, two
yeast nuclear genes coding for mitochondrial ribosomal proteins.";
J. Biol. Chem. 262:3388-3397(1987).
-I- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
                                                                                                                                                                                             EMBL; M15189; AAA34977.1; -. EMBL; U25840; AAB68152.1; -. EMBL; M15161; AAA74729.1; -. PIR; A26587; TVBYH1.
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STRAIN-$288c / AB972;
MEDLINE-97313271; PubMed-9169875;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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"Characterization of two members of the rho gene
yeast Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 84:779-783(1987).
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RHO1 OR YPR165W OR P9325.3.
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                                                                                                                HSSP; P06749; 1FTN.
SGD; S0006369; RHO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 387:103-105(1997).
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InterPro;
                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
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                                    IPR003578; GTPase_Rho.
IPR001230; Prenyl_site
    IPR001806;
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RESULT 40
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                                                                                                                                                                                                                                                                                                                     PIR; JQ1133; JQ1133.
InterPro; IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1.
Hypothetical protein; Transposable element; Transposition; DNA-binding; DNA recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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GTP (BY SIMILARITY).

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SEQUENCE (By similarity).
-:- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Burkholderia.
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                                                                                                                                                                                                                                                       FLIZ_BACSU
P35536;
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                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                  Flagellar biosynthetic FLIZ OR CHEA.
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NCBI_TaxID=6087;
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POTENTIAL.
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50 AA APPROXIMATE REPEATS
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gene,
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter M.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujlta M., Fujlta Y., Fuma S., Gallzri A., Galleron N.,
RA Fritz C., Fujlta M., Fujlta Y., Fuma S., Gallzri A., Galleron N.,
RA Hilbert H., Halsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Persecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Tamakoshi A., Tanaka T., Texpstra P., Tognoni A.,
RA Viati A., Wambutt R., Wedler E., Wedler E., Wedler E., Wedler E., Vasamoto K., Yata K.,
RA Viati A., Wambutt R., Vanamoto H., Yamane K., Yata K.,
RA Viati A., Seror S., Schroeter R., Vata K.,
RA Viati A., Vasamoto K., Vata M., Vanamoto K., Yata K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M87005; AAA22452.1;
EMBL; Z99112; CAB13507.1;
PIR; B41886; B41886.
SubtiList; BG10259; fliz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:249-256(1997).

-!- FUNCTION: MAY BE A STRUCTURAL COMPONENT OF THE FLAGELLUM THAT ANCHORS THE ROD TO THE MEMBRANE.

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes flip and fliz.":
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                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                             Flagella;
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210 GKKKGP 215
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                                                                  GKKKGP 55
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                                                                                                                                        Similarity 6; Conserv
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24871
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RESULT 42

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RESULT 43
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GN RPS3AE
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"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
-I- FUNCTION: EXCISES URACIL RESIDUES FROM THE DNA WHICH CAN ARISE
AS A RESULT OF MISLNCORPORATION OF DUMP RESIDUES BY DNA
POLYMERASE OR DUE TO DEAMINATION OF CYTOSINE (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).
-I- SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein SJAe.
                                                                                                                                                                                                                                                                                                                                                                        RS3A_PYRAE
Q8ZT21;
                                                                                                                              Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum. NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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     Fitz-Gibbon
                                PubMed=11792869;
                                                     SEQUENCE FROM N.A. STRAIN-IM2 / ATCC
                                                                                                                                                                                                               Pyrobaculum aerophilum.
                                                                                                                                                                                                                                       RPS3AE OR PAE3472
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DNA repair; Hydrolase; Glycosidase; Complete proteome.

ACT_SITE 61 61 GENERAL BASE (BY SIMILARITY).

SEQUENCE 220 AA; 25653 MW; AEAF19BEE0A2942C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR002043; U_DNA_giycsylse. InterPro; IPR003249; U_glycosyl. Pfam; PF03167; UDG; 1. ProDom; PD001589; U_glycosyl; 1. TIGRRAMS; TIGR00628; ung; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uracil-DNA glycosylase (EC UNG OR BU183.
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  Ladner H., Kim U.-J., Stetter K.O.,
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RESULT 44
YJO8_YEAST
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Query Match
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01-FEB-1996 (Rel. 33, I
01-OCT-1996 (Rel. 34, I
Hypothetical 26.9 kDa p
YJL148W OR J0637.
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                             Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.; "Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome x reveals 14 known genes and 13 new open reading frames including homologues of genes clustered on the right arm of chromosome XI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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P47006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01015; Ribosomal_S3Ae; 1.
ProDom; PD003035; Ribosomal_S3AE; 1.
PROSITE; PS01191; RIBOSOMAL_S3AE; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
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                                                             DOMAIN
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DOMAIN
                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                      or send an email to license@isb-sib.ch).
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nes 6; Conserv
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                                                                                                            S0003684; YJL148W
                                                                                                                           Z49423; CAA89443.1;
X87371; CAA60807.1;
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protein in INO1-IDS2
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Score 6;
                             POLY-LYS.
DCD42DFEC574EDB6 CRC64;
                                                             POLY-LYS.
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Q94051;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1998
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Swinburne J.;

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: MAY ACT AS A SCAFFOLDING PROTEIN WITHIN CAVEOLAR MEMBRANES. INTERACTS DIRECTLY WITH G-PROTEIN ALPHA SUBUNITS AND CAN FUNCTIONALLY REGULATE THEIR ACTIVITY.

- SUBUNIT: HOMOOLIGOMER COMTAINING 14-16 MONOMERS PER OLIGOMER.

- SUBGLILULAR LOCATION: MEMBRANE PROTEIN OF CAVEOLAE. POTENTIAL HAIRPIN-LIKE STRUCTURE IN THE MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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STRAIN-Bristol N2;
MEDLINE-97153022; PubMed-8999956;
Tang Z., Okamoto T., Boontrakulpoontawee P.,
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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J. Biol. Chem. 272:2437-2445(1997).
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                               InterPro; IPR001612; Caveolin.

Pfam; Pr01146; Caveolin; 1.

PROSITE; PS01210; CAVEOLIN; FALSE_NEG.

Pransmembrane; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z81122; CAB03359.1; -. WormPep; T13F2.8; CE13633.
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TFGKKK 51
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
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235 C
234 P
26291 MW;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PALMITATE (POTENTIAL).
F07B12DEB4D6F13A CRC64;
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Pred. No. 56;
0; Mismatches
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Search completed: February Job time : 14 secs 6, 2003, 21:31:12

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RESULT 25
US-09-764-855-113
Sequence 113, Application US/09764855
Patent NO. US20020119919A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA110
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US-09-764-869-1228
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US-09-764-869-1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 2442 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1228
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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SEQ ID NO 479
LENGTH: 51
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,855 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR EILING DATE: EARLIER FILING DATE: 1997-09-12 PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: LARLIER FILING DATE: 1997-09-12 NUMBER: PRIOR FILING DATE: BARLIER FILING DATE: 1997-09-12
                                                                                                                 Prior application data removed - NUMBER OF SEQ ID NOS: 334
                                   LENGTH: 55
TYPE: PRT
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              ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                     24 KKKKKT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 6; DB 1
%; Pred. No. 29;
0; Mismatches
                                                                                                                                  consult PALM or file wrapper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
28;
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TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: AGOMICA-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/2180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-06
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 67/236,359
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 601
LENGTH: 56
TYPE: PRT
TYPE: PRT
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Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47593, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                APPLICATION NUMBER: PCT/US01/00667
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Similarity 100.0%;
6; Conservative
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Similarity 100.0%
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank, David R.
Hanzel, David K.
Chen, Wensheng
2001-01-30
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b; Pred. No. 30;
0; Mismatches
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3; Pred. No. 30;
0; Mismatches
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR REPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-010-04

PRIOR FILING DATE: 2000-010-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04
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; FEATURE:
; FEATURE:
; OTHER INFORMATION: MAP TO AL049694.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.80
; OTHER INFORMATION: EXPRESSED IN HIBLIOO, SIGNAL = 0.88
; OTHER INFORMATION: SWISSPROT HIT: BF344101.1, EVALUE 8.00e-14
; OTHER INFORMATION: EST_HUMAN HIT: BF344101.1, EVALUE 8.00e-14
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Best Local Similarity
"heches 6; Conserve
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US-09-864-761-47812
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47593
LENGTH: 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                       APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION
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lo. 31;
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Pluta, Jason
APPLICANT: Ghosh, Malavika
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and
FILE REFERENCE: DEX-0289
CURRENT APPLICATION NUMBER: US/09/989,919
CURRENT APPLICATION NUMBER: 60/252,505
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.1
SEQ ID NO 118
LENCTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: MAP TO AC010290.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EST_HUMAN HIT: BE244981.1, EVALUE 1.00e-12
US-09-864-761-47812
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-919-118
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US-09-989-919-118
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOPTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47812
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. US20020164344A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 118,
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Best Local :
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OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00662
OR APPLICATION NUMBER: PCT/US01/00661
OR APPLICATION NUMBER: PCT/US01/00661
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09989919
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100.0%; Pr
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b; Pred. No. 32;
0; Mismatches
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5. 32;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 31
US-09-925-301-1475
; Sequence 1475, Application US/09925301
; Patent No. US20020052308A1
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US-09-925-300-1198
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                         SEQ ID NO 1475
LENGTH: 62
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Best Local Similarity
IOCATION: (8)
OTHER INFORMATION: X
NAME/KEY: SITE
NAME/KEY: (9)
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
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TYPE: PRT
                                                                                    NAME/KEY: SITE LOCATION: (5)
OTHER INFORMATION:
                                                                                                                               NAME/KEY: SITE LOCATION: (3)
OTHER INFORMATION:
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                               FEATURE:
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                                        Xaa equals any of the naturally occurring L-amino acids
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                                                               US-10-117-604-2
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US-10-117-604-2
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      Matches
                  Query Match
Best Local
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                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/117,604
FILING DATE: 04-Apr-2002
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: US/08/971,089
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/030,987
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            NAME: Ramos, Robert T.
REGISTRATION NUMBER: 37,915
REFERENCE/DOCKET NUMBER: P-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619,535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive,
                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID ENCODING
SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pulst, Stefan M.
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      Similarity 100 6; Conservative
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6; Conserv
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COUNTRY: United States
                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                   TELEFAX: (619)535-8949
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100.0%; Pr
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                                                                               SEQ
                  Score 6; I
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Pred. No
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33;
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23 EKKKKK 28

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US-09-764-846-260; Sequence 260, Application US/09764846; Patent No. US20020102638A1
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Best Local Similarity
Thes 6; Conserve
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                                                                                                                                                                  PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669
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APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
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NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR FILING DATE: 2000-09-27
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TYPE: PRT
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                APPLICATION NUMBER: PCT/US01/00665
FILLING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILLING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILLING DATE: 2001-01-30
                                                                                                                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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ilarity 100.0%;
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Pred. No. 33;
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RESULT 36
US-09-764-877-1089
; Sequence 1089, Application US/09764877
; Patent No. US20020147140A1
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                               GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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LENGTH: 66
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Best Local Similarity
Matches 6; Conserv
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45501
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ12
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
Prior application data removed - refer to NUMBER OF SEQ ID NOS: 4031
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TYPE: PRT
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.56
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
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les 6; Conserv
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100.0%; Pr
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Pred. No.
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Sequence 18, Application US/09201936

Publication No. US20020187946A1

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003

CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: US/09/201,936

CURRENT FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER: 09 501,485
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Best Local Similarity
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US-09-867-550-284
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 284
LENGTH: 67
TYPE: PRT
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APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR APPLICATION NUMBER: USSN 60/208,427
NUMBER OF SEQ ID NOS: 2125
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Pred. No. 35;
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RESULT 40
US-09-764-846-191
US-09-764-846-191
Sequence 191, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ12
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
EARLIER FILING DATE: 1995-08-04
EARLIER FILING DATE: 1995-08-04
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Best Local Similarity
Thes 6; Conserv
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Best Local S
Matches 6
                                                Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 191
LENGTH: 68
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
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Publication No. US20020187946A1
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APPLICANT: MacKenzie, Alexande
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
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TYPE: PRT
ORGANISM: Homo sapiens FEATURE:
                                    TYPE: PRT
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nes 6; Conserv
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100.0%; Pred. No. 35
Live 0; Mismatches
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RESULT 42
US-09-764-846-179
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Sequence 1340, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
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Matches 6
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1340
LENGTH: 69
TYPE: "---
                                                                      Sequence 179, Application US/09764846 Patent No. US20020102638A1
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Matches
                                                        GENERAL INFORMATION:
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              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ12
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
CURRENT APPLICATION NUMBER: US/09/764,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA102
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OTHER INFORMATION: Xaa
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NAME/KEY: SITE
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GENERAL INFORMATION: APPLICANT: Rosen et al.

SOFTWARE: PatentIn Ver. SEQ ID NO 242 LENGTH: 73

Prior application data removed - NUMBER OF SEQ ID NOS: 348

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and

Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PT212 CURRENT APPLICATION NUMBER: US/09/764,846 CURRENT FILING DATE: 2001-01-17

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US-09-764-846-242
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SEQ ID NO 1105
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local S
Matches 6
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Sequence 242, Application US/09764846 Patent No. US20020102638A1
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SEQ ID NO 179
LENGTH: 72
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                                                                                                                                               Matches
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001
Prior application data ren
NUMBER OF SEQ ID NOS: 348
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TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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RESULT 45
US-09-833-067-9
iSequence 9, Application US/09833067
iSequence 9, Application US/09833067
iSequence 9, Application US/09833067
iSequence 9, Application US/09833067
iSequence 9, Application US200208488A1
iGeneral Information: Descript Pill, Their Production and USE TITLE OF INVENTION: DISSOCIATED PILI, THEIR PRODUCTION AND USE FILE REFERENCE: 050939/0102
iCURRENT FILING DATE: 2000-04-12
iCURRENT FILING DATE: 2000-04-12
iPRIOR APPLICATION NUMBER: 60/196.493
iPRIOR FILING DATE: 2000-04-12
iNUMBER OF SEQ ID NOS: 26
iSoftware: Patentin Ver. 2.1
iSEQ ID NO 9
iLENGTH: 75
iTYPE: PRT
iCRANISM: Artificial Sequence
iPEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
iCOTHER INFORMATION: sequence of papH gene deletion mutant
US-09-833-067-9
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; ORGANISM: Homo sapiens
US-09-764-846-242
Search completed: February 6, 2003, 21:32:50 Job time : 12 secs
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26 ARAGKV 31
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Maximum DB
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pir4:*
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ALIGNMENTS

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C;Species: Homo Sapiens (Man)
C;Date: 30-Sep:1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C;Date: 30-Sep:1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C;Accession: JC1278; I37387; S68911; S21449; S21450
R;Kas, K.; Michiels, L.; Merregaert, J.
Blochem. Biophys. Res. Commun. 187, 927-933, 1992
A;Title: Genomic structure and expression of the human fau gene: Encoding the ribo A;Reference number: JC1278; MUID:92412144; PMID:1326960
A;Recession: JC1278
A;Residues: 1-133 <KAS-
A;Residues: 1-133 <KAS-
A;Cross-references: EMBL:X65921; NID:931304; PIDN:CAN46714.1; PID:931305
A;Cross-references: EMBL:X65921; NID:931304; PIDN:CAN46714.1; PID:931305
Oncogene 8, 2537-2546, 1993
A;Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as
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A;Accession: B47416
A;Accession
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J. Biol. Chem. 268, 17967-17974, 1993
A;Title: The carboxyl extension of a ubiquitin-like protein is A;Reference number: A47416; MUID:93352612; PMID:8394356
A;Accession: A47416
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JC1278
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A; Residues: 1-133 <OLV>
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Pred. No. 5.2e-52;
1; Mismatches 0;
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A; Gene: fau
A; Introns: 25/3;
C; Superfamily: u
F; 1-74/Domain: u
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A.Status: preliminary
A.Rolecule type: DNA
A.Rolec
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C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
C:Accession: 148346; A56532; T59368; S21452
R.Michiels, L.; Van der Rauwelaert, E.; Van Hasselt, F.; Kas, K.
Oncogene 8, 2537-2546, 1993
A:Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein an A;Reference number: 137387; MUID:93368957; PMID:8395683
A;Accession: 148346
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Gene: fau
A;Gene: fau
A;Introns: 25/3; 74/1; 92/3
A;Introns: 25/3; 74/1; 92/3
C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
C;Keywords: protein biosynthesis; ribosome
F;1-74/Domain: ubiquitin homology <UBH>
F;75-133/Product: ribosomal protein S30, cytosolic #status experimental <MAT>
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R;Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede, Eur. J. Biochem. 239, 144-149, 1996
A;Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal and A;Reference number: S68911; MUID:96305378; PMID:8706699
A;Accession: S68911
A;Molecule type: protein
A;Residues: 75-99 <VLA>
C;Genetics:
                                                                                                                                                                                                                                                    A;Cross references: GB:D26610; NID:g1060926; C;Genetics:
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Genomics 25, 291-294, 1995
A;Title: The mouse Fau gene:
A;Reference number: A5632; N
A;Accession: A56532
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A;Accession: 137387
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-133 <RES>
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A; Residues: 1-133 < RE2>
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Best Local Similarity
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                                                                                                                                                                                       25/3; 74/1; 92/3
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                                                  SEB4B protein - human (fragme
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence
C;Accession: S38383
                                                                                                                                                                                       RESULT
S38383
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A;Gene 142g19750
A;Map position: 2
C:Superfamily: yeast ribosomal protein S30
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                                                                                                                                                                                                                                                                                                                                                   KVHGSLARAGKVRGQTPKVAKQ 22
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Similarity

37.3%; 500 100.0%; Pr

Score 22; Pred. No.

DB 2; I 4.7e-15;

Length 68

Mismatches

0

0,

Gaps

0

Conservative

30

human (fragment)

#sequence_revision

06-Feb-1995

#text_change

08-Sep-1997

Gupta,

A.; Terworst,

<u>ر</u>

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A;Title: Sequence and ar
A;Reference number: A84A
A;Reference number: A84A
A;Accession: F84580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <STO>
A;Cross:references: GB:/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: (C;Genetics: A;Gene: AT4g29390 A;Map position: 4
                                                                                                                                             euss, D.; Nierman, W.C.; V
Nature 402, 761-768, 1999
                                                                                                                                                                             R;Lin, X.; Kaul, S.;
M.; Koo, H.; Moffat,
                                                                                                                                                                                                                       40S ribosomal protein S30 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_chc;Accession: F84580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A85001;
A;Accession: H85342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIBOSOMAL PROTEIN S30 homolog (imported) - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: H85342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; anonymous, The Euro
Nature 402, 769-777,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 22
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22; Conserv
                                                                                                                                                              S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. fat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Union Arabidopsis Genome Sequencing Consortium, 77, 1999
                                                                                                     nd analysis of chromosome 2 of the plant A84420; MUID:20083487; PMID:10617197
    GB:AE002093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:NC_001268;
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    NID: g3687243; PIDN: AAC62141.1;
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4.3e-1
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                                                                                                                                                                                                                                               #text_change 17-May-2002
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                                                                                                                        Arabidopsis thaliana
      GSPDB:GN00139
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                                                                                                                                                                   Venter
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A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: A71604
                                                                                                                                                                                                                                          R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite 1
                                                                                                                                                                                                                                                                                                                          ribosomal protein S30 PFB0885w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 13-Aug-1999 C;Accession: A71604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C;Accession: T15642
                                                                                  A; Experimental source: C; Genetics:
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C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: The sequence
A;Reference number: Z18381
A;Accession: T15642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Geisel, C.; Stellyes, L.; Bradshaw, H. submitted to the EMBL Data Library, March 1996 A;Description: The sequence of C. elegans cosm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-229 <RUE>
A; Cross-references: EMBL: X75315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S38382
A; Accession: S38383
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                                                                                                                          A; Cross-references:
                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-58 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP:C26F1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-130 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA
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13; Conser
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llarity 100.0%; Pred. No. 1.3e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                        ribosomal protein
                                                                                                   :AE001422;
clone 3D7
                                                                                                                                                                                   nucleic acid
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  20.3%;
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                                                                                                                      GB:AE001362;
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Score 12;
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                                                                                                                                                                                 sequence not shown;
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, 8.9e-06;
  DВ
                                                                                                                      NID:g3845298; PIDN:AAC71966.1; PID:g38453
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Length 58;
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                                                                                                                                                                               translation not shown
                                                                                                                                                                                                                                                                                  Aravind, L.; Koonin, R.; White, O.; Smith
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C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Ju1-2000
C;Accession: S670774; S70775; S70776; S70774
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                             R;Baker, R.T.; Williamson, N.A.; Wettenhall, R.E.H.
J. Biol. Chem. 271, 13549-13555, 1996
A;Title: The yeast homolog of mammalian ribosomal protein A;Reference number: S70774; MUID:96278780; PMID:8662789
A;Accession: S70775
                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z75090; GSPDB:GN00015; MIPS:YOR182c; NID:g1420438; PIDN:CAA:A;Experimental source: strain S288C
A;Genetics: YS30B
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A; Introns: 13/3; 56/3
C; Superfamily: yeast
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T39834
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C; Genetics: <YS30B>
                     A; Molecule type: protein A; Residues: 2-63 < BA3>
                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-63 < BAW>
                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-63 <BAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: S67074
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A; Residues: 1-61 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z21884
A; Accession: T39834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
                   A; Residues:
                                                                   A; Accession:
                                                                                           A; Genetics: YS30A
                                                                                                         A;Cross-references: EMBL:U48699;
                                                                                                                                                                                   A; Accession: S70776
                                                                                                                                                                                                           A; Genetics: YS30A
                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A: Molecule type: DNA
A: Residues: 1-63 < HUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein S30.e, cytosolic - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O4725; protein YLR287c-a; protein YOR182c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL021839; PIDN:CAA17057.2; GSPDB:GN00067; SPDB:SPBC19G7.03c
A;Experimental source: strain 972h-; cosmid c19G7
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Best Local :
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nes 12; Conserv
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                                                                                                                                                                                                                              EMBL: U48700;
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; Pred. No.
                                                                                                                NID:g1256750; PIDN:AAC49316.1; PID:g1256751
                                                                                                                                                                                                                              NID:g1256752; PIDN:AAC49317.1; PID:g1256753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein YLR287c-a;
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; Mismatches 0;
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:RPS30B; MIPS:YOR182c

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A; Molecule type: DNA
A; Residues: 1-134 <LA1>
C; Genetics:
A; Gene: hns
C; Function:
A; Description: binds doul
C; Superfamily: DNA-bindi
C; Keywords: DNA binding;
                                                                                                                                                                                                                      K; La Teana, A.; Falconi, M.; Scarlato, V.; Lammi, M.; Pon, C.L.
FEBS Lett. 244, 34-38, 1989
A; Title: Characterization of the structural genes for the DNA-binding protein H-NS
A; Reference number: S02775; MUID:89171270; PMID:2494066
A; Accession: S02776
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A;Map position: 15R
A;Introns: 1/3
C;Genetics: <YS30A>
A;Gene: SGD:RPS30A; N
A;Cross-references: 1
                                                                                                                                                                                                                                                                                                                  C:Species: Proteus vulgaris
C:Date: 28-Feb-1990 #sequence_revision
C:Accession: S02776
                                                                                                                                                                                                         A; Status: not compared with
                                                                                                                                                                                                                                                                                                                                                 DNA-binding protein H-NS - Proteus vulgaris C:Species: Proteus vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: GB:AE001437; PIDN:AAK79540.1; PID:g15024526; GSPDB:GN00168 A:Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uncharacterized protein, VJDF B. subtilis ortholog [imported] - Clostridium acetobutylic C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: A97094
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A.Map position: 12R
A.Introns: 1/3
A.Introns: 1/3
C.Superfamily: yeast ribosomal protein S30.e
C.Keywords: cytosol; protein biosynthesis; ribosome
F,2-63/Product: ribosomal protein S30.e, cytosolic #status experimental <MAT>
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A; Residues: 1-135 < KUR>
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Matches 12
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Best Local
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     Local Similarity
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                                                                        binds double-stranded DNA; influences DNA-binding protein H-NS
                                                         binding;
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MIPS:YLR287c-a;
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                                                     transcription regulation
   100.0%;
                       11.9%;
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                                                                                                                                                                                                       conceptual translation
Score 7;
Pred. No.
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Pred. No. 0.9
0; Mismatches
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Pred. No.
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No.
                                                                                                                                                                                                                                                                                                                                28-Feb-1990 #text_change
DB 2;
o. 9.8;
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               Length 134
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                                                                                          regulation of
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                                                                                      gene expression at tr
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nucleoporin p62 homolog - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 05-Nov-1999
                                                                  RESULT
I52523
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                                                                                                                                        B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
E84782
                                                                                                                                                                                                                                                                              A; Map position:
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A; Residues: 1-199 <STO>
                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable homeodomain transcription factor [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: E84782
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C. Species: Deinococcus radiodurans
C. Date: 03.0ec.1999 #sequence_revision 03.Dec.1999 #text_change 31.Mar-2000
C. Accession: B75305
R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                      A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
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A; Residues: 1-154 <WHI>
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osition: 2
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                                                                                                                                                                                                     11.9%;
100.0%;
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T.; Zalewski,
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probable 60S ribosomal protein L6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H86318
C;Accession: H86318
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon:
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Junkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Junkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia:
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Coccession: H86318
A;Residues: 1-233 <STO>
A;Coccession: Researcher Circumptor of the plant Arabidopsis.
A;Coccession: R
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R;Wang, Z.Q; Akmal, K.M.; Kim, K.H.
Biol. Reprod. 51, 1022-1030, 1994
A;Title: An unusual nucleoporin-related messenger ribonucleic acid is present in A:Reference number: I52523; MUID:95151924; PMID:7849178
A;Accession: I52523; MUID:95151924; PMID:7849178
A;Accession: I52523
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Residues: 1-215 <RES>
A;Residues: 1-215 <RES>
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, i. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                          protein 60S ribosomal protein L6 F2P9.8 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96768 R;TheoLogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000
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C;Genetics:
A;Map position: 1
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100.0%;
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s; Pred. No. 15;
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                   C.J.; Federspiel, N.A.; Kaul, S.; White, (Conway, A.B.; Conway, A.R.; Creasy, T.H.;
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o. 15;
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o. 14;
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                                                                                                                                          Tallon,
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war, K.;
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submitted to the Protein Sequence Databa
A; Reference number: Z24376
A; Accession: T47174
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-283 <AAA>
A; Cross references: EMBL: AL162072
A; Experimental source: adult melanoma (MC; Genetics: DKFZp7621166.1
C; Superfamily: unassigned WD repeat prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
A; Gene: F2P9.7
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rytheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: E96768
A; Accession: E96768
A; Status: preliminary
A. Molocule trace, NAA
                                                                                                                                                                                                                                                                                                                   hypothetical protein DKFZp762I166.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T47174
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, S.
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A;Molecule type: DNA
A;Residues: 1-233 <STO>
A;Residues: 1-233 <STO>
A;Cross-references: GB:AE005173; NID:g7109467; PIDN:AAF36731.1; GSPDB:GN00141
C;Genetics:
A;Gene: F299.8
A;Map position: 1
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A; Residues: 1-233 <STO>
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Best Local (
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Best Local
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                                                                  unassigned WD repeat proteins; WD repeat homology
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                                                                                                                                                                                                                                                                                                Sequence Database,
11.9%;
100.0%;
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Score 7;
Pred. No
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Pred. No.
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Pred. No.
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                                                                                                                                     (MeWo cell line); clone DKFZp762I166
DB 2;
o. 18;
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15;
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                     Length 283
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Similarity

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probable ABC-type transport system ATP-binding protein -
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_
C;Accession: T36154
R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barr
                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C32A3.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T19629
R; Thomas, K
submitted to the EMBL Data Library, February 1995
A; Reference number: Z19154
A; Accession: T19629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 21
T19629
                                                                                                                                                                                                                                                                   A; Map position: 3
A: Introns: 47/3; 79/3;
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                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z48241; PIDN:CAA88285.1; GSPDB:GN00021; CESP:C32A3.2
A;Experimental source: clone C32A3
                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-346 <WIL>
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C;Speciles: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Sep-1999
C;Accession: D70313
                                                                                                                                                                                                                                                                                                       A; Gene: CESP: C32A3.2
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C;Superfamily: conserved
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A; Residues: 1-314 <AQF>
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A;Accession: D70313
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                                #text_change 03-Dec-1999
                                                                                                                                                                                                         0;
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   Barrell,
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                                                          Streptomyces coelicolor
 B.G.;
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Best Loc
Matches
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                Local
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submitted to the EMBL Data Library, July 1999
A; Reference number: Z21598
A; Accession: T36154
A; Status: preliminary; translated from GB/EMBL/I
A; Molecule type: DNA
A; Residues: 1-424 <SEE>
A; Cross-references: EMBL:AL096852; PIDN:CAB5101:
A; Experimental source: Strain A3(2)
C; Genetics:
C; Genetics:
                                                                                                                        A;Status: present DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecules: 1-710 <SCH> A;Molecules: 1-710 <SCH> A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.680 A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.680 A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.680
                                                                                                                                                                                                                                                                                                        R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                           C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                              Atu related protein [imported] - Neu N;Alternate names: protein B14D6.680
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C;Superfamily: phage P22 gene 12 protein
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A; Molecule type: DNA
A; Residues: 1-454 <STO>
A; Cross-references: GB:AP001520; GB:BA0000004; NID:g10176401; PIDN:BAB07748.1;
A; Cross-imental source: Strain C-125
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A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodu: A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E84153
                                                                                  A; Introns: 422/1
                                                                                                       A; Map position:
                                                                                                                                                                                                                                             A; Status: preliminary
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Matches 7
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Similarity 7; Conserv
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                     Score 7; Pred. No.
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                     DB 2;
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Conservative

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Mismatches

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Gaps

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1254 <SNE>
A; Cross-references: GB:L0459; NID:g290619; PIDN:AAA42990.1; PID:g290621
C; Superfamily: togavirus structural polyprotein
C; Keywords: coat protein; glycoprotein; predicted <CTP>
F; 274/Product: membrane glycoprotein E3 #status predicted <MG3>
F; 275-333/Product: membrane glycoprotein E2 #status predicted <MG2>
F; 701-721/Domain: transmembrane #status predicted <TMI>
F; 757-812/Product: 6K protein #status predicted <TMI>
F; 794-813/Domain: transmembrane #status predicted <TMI>
F; 794-813/Domain: transmembrane #status predicted <TMI>
F; 813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>
F; 794-813/Domain: transmembrane #status predicted <TMI>
F; 813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>
F; 794-813/Domain: transmembrane #status predicted <MG1>
F; 1731-1248/Domain: transmembrane #status predicted <MG1>
F; 1731-1248/Domain: transmembrane #status predicted <MG1>
F; 1731-1248/Domain: transmembrane #status predicted <MG1>
F; 1751-5148/Domain: transmembrane #status predicted <MG1>
F; 1751-514/Product: membrane #status predicted <MG1>
F;
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J. Gen. Virol. 74, 519-523, 1993
A;Title: Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB vi A;Reference number: JQ1978; MUID:93187617; PMID:8445371
A;Accession: JQ1979
A;Accession: JQ1979
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A;Map position: 4
C;Superfamily: unassigned Ser/Thr or Tyr-specific
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RESULT
B71619
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A; Residues: 1-863 <STO>
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C;Accession: B69830

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F.; Ogasawara, N.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, T. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, Authors: Laber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Mauthors: Laber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Mauthors: Schleich, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scani, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scani, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
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A; Map po
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                                                                                                                                                                                                                                                                                                                                                           hypothetical protein yhfD - Bacillus subtilis
C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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A; Reference number: Z20525
A; Accession: T28799
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
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A;Experimental source: strain Bristol N2; clone C16E9
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A; Residues: 1-46 <GEI>
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R;Geisel, C.
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A;Residues: 1-2539 <GAR>
A;Cross-references: GB:AE001384; GB:AE001362; NID:g3845139; PIDN:AAC71845.1; PID:g384
A;Experimental source: clone 3D7
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C;Species: Plasmodium falciparum
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hypothetical protein T22K7.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Datc: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47/434
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; L
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24459
A;Accession: T47/434
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <RIE>
A;Cross-references: EMBL:AL138641
A;Experimental source: cultivar Columbia; BAC clone T22K7
C;Genetics:
A;Map position: 3
A;Introns: 31/3
A;Note: T2ZK7.120
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C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_viiiing
C;Accession: H97135
R;Molling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.;
Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97135
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A; Residues: 1-70 < KUR>
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A;Gene: yhfD
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A; Residues: 1-67 < KUN>
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A;Experimental source: strain 168
A;Note: 20-Asp was also found
A;Note: 20-Asp was also found
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                        A; Molecule type: protein A; Residues: 4-26 <HIG>
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Query Match

10.2%;

Score

6,

DВ <u>ب</u>

Length 74;

A; Authors: Foulger, D.; Fritz, C.; iech, J.; Harwood, C.R.; Henaut, A

.; Fujita, M.; Fujita, Y.; Fuma, A.; Hilbert, H.; Holsappel, S.;

S.; Galizzi, Hosono, S.;

Hullo,

A.; Gal

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ribosomal protein S18 (rpsR) - Bacillus subtilis
N;Alternate names: ribosomal protein BS21
C;Species: Bacillus subtilis
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S66013; S11368; A69701
R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
BNA Res. 1, 1-14, 1994
A;Reference number: S65967; MUID:96051385; PMID:7584024
A;Accession: S66013
A;Experimental source: strain 168
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
R;H190, K.I.; Otaka, E.; Osawa, S.
MOI. Gen. Genet. 185, 239-244, 1982
A;Title: Purification and characterization of 30S ribosomal proteins from Bacillus su A;Reference number: S09561; MUID:82219212; PMID:6806564
A;Accession: S11368
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A; Molecule type: DNA
A; Residues: 1-80 <HEI>
A; Residues: 1-80 <HEI>
A; Cross-references: GB: AE004173; GB: AE003852; NID: g9655341;
A; Cross-references: serogroup O1; strain N16961; biotype
                                                                                                                                                      A; Cross-references: EMBL: D26185; NID: 9467326; PIDN: BAA05219.1; PID: 9467373
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A; Residues: 1-81 <OGA>
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C; Superfamily: exodeoxyribonuclease VII small
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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transcription regulator XFa0057 [imported] - Xylella fastidiosa (strain 9a5c C.Species: Xylella fastidiosa C.Species: Xylella fastidiosa C.Species: Aug-2000 *sequence_revision 20-Aug-2000 *text_change 02-Sep-2000 C.Accession: H82867
R.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000
A.Yiltle: The genome sequence of the plant pathogen Xylella fastidiosa.
A.YReference number: A82515; MUID:20365717; PMID:10910347
A.Rocession: H82867
A.Rocession: H82867
A.Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-Jan-2001 C;Accession: T36134 R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, July 1999 A;Reference number: Z21598 A;Reference number: Z21598 A;Accession: T36134
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A;Gene: rpsR
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A;Residues: 1-81 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16126.1; PID:g2636636
A;Experimental source: strain 168
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A; Residues: 1-92 <SEE>
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Familv: probable sulfur carrier protein s1r0821
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Pred. No.
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H96585

H96585

C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Date: (02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96585
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn. L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Kalzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Recession: H96585
A;Accession: H96585
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A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fi J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kriteger, J.E.; Kuramae, E.E.; Le chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawe, A.; Stuthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.F.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A.; Reference number: A59328
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A;Residues: 1-92 <SIM-A;Residues: 1-92 <SIM-A
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A; Residues: 1-98 <STO>
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                                                                                                                                                                     10.2%; Score 6; DB | 100.0%; Pred. No. 76 | tive 0; Mismatches
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100.0%; Pred. No.
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Maiti, R.;
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RESULT 37
T07078
cold stress protein SRC1 - soybe
C:Species: Glycine max (soybean)
C:Date: 30-Apr-1999 #sequence_re
C:Accession: T07078

#sequence_revision

30-Apr-1999 #text_change

20-Jun-2000

soybean

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hypothetical protein 105 (grm 3' region) - Micromonospora purpurea (fragment) C; Species: Micromonospora purpurea C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994 C; Accession: PW0017 R; Kelemen, G.H.; Cundliffe, E.; Financsek, I. Gene 98, 53-60, 1991 Gene 98, 53-60, 1991 A; Title: Cloning and characterization of gentamicin-resistance genes from Mic. A; Recession: PW0017 A; MUID:91192615; PMID:2013410 A; Accession: PW0017 A; Molecula type: DNA A; Residues: 1-105 < KEL> RESIDUES: 1-105 < KEL> RESIDUES: MICROMON A; RESIDUES: MICROMON A; RESIDUES: 1-105 < KEL> RESIDUES: 1-105 < KEL> RESIDUES: MICROMON A; RESIDUES: MICROMON A; RESIDUES: 1-105 < KEL> RESIDUES: MICROMON A; RESIDUES: MICROMON A; RESIDUES: 1-105 < KEL> RESIDUES: MICROMON A; RESIDUES: MICROM
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87604
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C;Superfamily: cold stress
C;Keywords: cold shock
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Plant Sci. 123, 93-104, 1997
A;Title: CDNA sequence analysis
A;Reference number: 215902
A;Accession: T07078
                                                                                               A; Note: the C; Keywords:
                                                                                                                                            A;Cross-references: GB:M55520
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A; Residues: 1-104 <S'
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    Matches
                                                                                               Keywords: antibiotic
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les 6; Conserv
                          Local
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                                                                                                                    Phe
                                                                                                                    and
                                                                                                                                                        hypothetical protein YMR290w-a - yeast C;Species: Saccharomyces cerevisiae C;Date: 23-Aug-1996 #sequence_revision C;Accession: S69849
R;Barrell, B.G.
                                                                                                                                                                                                                                                                             RESULT 42
S69849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-106 <CALY
A;Cross-references: EMBL:L39005; NID:g625154; PIDN:AAA99963.1; PID:g625155
A;Experimental source: seedling; tissue type leaf
C;Superfamily: cold stress protein COR19
C;Keywords: cold shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Cai, Q.: Moore, G.A.; Guy, C.L.
Plant Mol. Biol. 29, 11-23, 1995
A:Title: An unusual group 2 LEA gene family in citrus responsive A; Reference number: S59534; MUID:96017610; PMID:7579157
A; Accession: S59536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Kelemen, G.H.; Cundliffe, E.; Financsek, I. Gene 98, 53-60, 1991
A;Title: Cloning and characterization of gentamicin-resistance A; Reference number: JG0017; MUID:91192615; PMID:2013410
A; Accession: PW0018
                                             A; Accession: S69849
A; Molecule type: DN
A; Residues: 1-115 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Poncirus
C; Date: 19-Mar-1997
C; Accession: S59536
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
C;Accession: PW0018
                                                                                                                submitted to the EMBL Data A; Reference number: S47445
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PW0018
                       A; Cross-references: EMBL: X80836;
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A; Residues: 1-105 <KEL>
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11 SLARAG
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Pred. No. 81;
0; Mismatches
                                                                                                                                     August 1994
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RESULT 43

H84651

hypothetical protein At2g25720 [imported] - Arabidopsis thaliana
C:Specles: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84651
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; I
R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, J.A.; Salzberg, S.L.; Fraser, C.:
                                                                                                                                                                                                     A;Cross-references: GB:AE001259; GB:AE000520; NID:g3323209; PIDN:AAC65861.1; PID:g332322
A;Experimental source: strain Nichols
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                            probable ribosomal protein L19 (rplS) - syphilis spirochete
c;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-ul-1998 #sequence_revision 24-Jul-1998 #text_change 13-Aug-1999
C;Accession: B71268
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
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                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome seq
A;Reference number: A71250;
A;Accession: B71268
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A;Gene: At2g25720
A;Map position: 2
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A; Residues: 1-117 <STO>
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C;Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-123 <COL>
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C; Superfamily: Saccharomyces hypothetical protein YMR290w-a
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                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                       sequence of Treponema pallidum, the syphilis spirochete 10; MUID:98332770; PMID:9665876
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A;Cross-references: EMBL:X62482; NID:g57723; PIDN:CAA44349.1; PID:g57724 A;Note: the protein is designated as ribosomal protein S25 by comparison C;Superfamily: rat ribosomal protein S25 C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal protein S25, cytosolic [validated] - rat C;Specles: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000 C;Accession: A38999; S17353 R;Chan, Y_L.; Wool, I.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 45
R3RT25
                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 186, 1688-1693, 1992
A;Title: The primary structure of rat ribosomal protein
A;Reference number: JH0691; MUID:92378645; PMID:1354961
A;Accession: A38969
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Search completed: February
Job time : 21 secs
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A; Residues: 1-125 <CH2>
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Best Local :
                                                                                   81 GSLARA
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100.0%; Pred. No.
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Q18231
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Q9NBB4
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Q920W8
Q920W7
Q91V99
Q90YP1
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                                               O9h5v4 homo sapien
O9jj24 mus musculu
O920w8 mus musculu
O920w7 mus spicile
O91v99 mus musculu
O90yp1 ictalurus p
O9m0e4 arabidopsis
O15351 homo sapien
O9vdh8 drosophila
O18231 caenorhabdi
O96241 spodoptera
       09s9j0 arabidopsis
097ir7 clostridium
091657 proteus mir
09rse5 deinococcus
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO2639; BAB15515.1; -.
HSSP; P02448; JUBI.
Interpro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0348; UBIQUITIN.
SMART; SM00213; UBC; 1.
PROSITE; PS0029; UBIQUITIN_1;
PROSITE; PS50053; UBIQUITIN_2;
SEQUENCE 133 AA; 14390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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        75
ch 100.0%; Score 59; DB 4; 1 1 Similarity 100.0%; Pred. No. 3.5e-56; 59; Conservative 0; Mismatches 0;
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5D2F81F2A355B559 CRC64;
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kelschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shlbata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y.:
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Best Local
Q920W8;
01-DEC-2001
                                    Q920W8
                                                                                                                                                                                                                                                   PROSITE; PS00299; UBIQUITIN_1; PROSITE; PS50053; UBIQUITIN_2; SEQUENCE 133 AA; 14416 MW;
                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AF147745; AAF80246.1; -.
EMBL; AK008466; BAB25684.1; -.
EMBL; AK002355; BAB22034.1; -.
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Q9JJ24;
01-OCT-2000
                                                                                                                                                                                                                                                                                                      PRINTS; PR00348; UBIQUITIN. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SWISS OB;
Nide G.-Y., Li Y., Salamonsen L.A., Clements J.A., Findlay J.K.;
"Identification of monoclonal non-specific suppressor factor beta
one of the genes differentially expressed at implantation sites
compared to interimplantation sites in the mouse uterus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai J., Shinagawa A., Shibata K., Yoshino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Mus musculus (Mouse).
Aberta; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal non-specific suppressor factor beta (Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed) (fox
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000626; Obiquitin.
                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:102547; Fau.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE, MEDLINE-21085660; PubMed-11217851;
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                                                                                                            PF00240; ubiquitin;
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(TrEMBLrel.
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                                   PRELIMINARY;
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Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
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Adachi J., Fukuda
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Q91V99;
Q91V99;
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                                                                                                                                                                                                                                                                                                                                            Mus spicilegus (Steppe mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                 Pfam; PF00240; ubiquitin; 1.
PROSITE; PS00299; UBIQUITIN_1;
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                                                                                                                                                                                                                                                            Five Mus musculus subspecies.
                                                                                                                                                                                                                                                             Liu Y., Kitano T., Kolde T., Shiroishi T., Moriwaki K., Saitou "Conspicuous Differences among Gene Genealogies of 21 Nuclear (Five Mus musculus subspecies.";
                                                                                                                                                                                                                                                                                               STRAIN-ZBN;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10103;
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mamumalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou "Conspicuous Differences among Gene Genealogies of 21 Nuclear C Five Mus musculus subspecies.":
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01-MAR-2002
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                                                                             1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGDNANS
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                                                                                                                               Similarity
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PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                  137 AA;
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                                                                                                                   Conservative
           PRELIMINARY;
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                                                                                                                                                                  14787 MW;
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Rodentia;
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Last annotation update)
         PRT;
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Pred. No. 3.6e-56;
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Pred. No. 3.6e-56;
                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
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Sciurognathi; Muridae; Murinae; Mus
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Submitted (FEB-2000) to the EMBI,
EMBI, AB039084; BAB68608; 1; -
EMBI, AB039085; BAB68609; 1; -
EMBI, AB039085; BAB68611; -
EMBI, AB039089; BAB68612; -
EMBI, AB039089; BAB68613; -
EMBI, AB039099; BAB68614; -
EMBI, AB039090; BAB68615; -
EMBI, AB039091; BAB68615; -
EMBI, AB039092; BAB68615; -
EMBI, AB039093; BAB68615; -
EMBI, AB039093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q90YP1 PRELIMINARY;
Q90YP1;
01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-MAR-2002 (TrEMBLrel. 20, L
408 ribosomal protein S30.
                                                                                                                                      Ribosomal
SEQUENCE
                                                                                                                                                                       Submitted (JUL-2001) to the EMBI
EMBL; AF402841; AAK95215.1; -.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PROSITE; PS50053; UBIQUITIN_2; :
                                                                                                                                                                                                                                                                         Karsi A., Patterson A., Feng J., Liu Z.J.;
"Translational machinery of channel catfish: I. A transcriptomic approach to the analysis of 32 40S ribosomal protein genes and the expression.";
                                                                                                                                                                                                                                                                                                                                                                                                             Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata
Actinopterygii; Neopterygii; Teleostei
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-VARIOUS STRAINS;
Liu Y., Kitano T., Koide T., Sh
"Conspicuous Differences among
"Conspicuous Differences among
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7998;
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QYNRREVNVVPTFGKKKGPNANS
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l Similarity 100.0%;
59; Conservative (
                                                           Similarity
23; Conser
                                                                                                                                      protein.
133 AA;
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                                                           Conservative
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                                                                                                                                      AA;
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                                                                                                                                    14504 MW;
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Last
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                                                                           Score 23;
Pred. No.
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Pred. No. 3.6
0; Mismatches
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                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                  Teleostei;
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                                                                                                                                    62036BB0E72C5CAC CRC64;
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hes 0;
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                                                                           4.1e-17;
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ogies of 21 N
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                                                                                             Length 133;
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O SHOULT ON SHOU
                                         Query Match
Best Local
             Matches
                                                                                                                                                               "Arabidopsis ORF clones.";

Submitted (OCT-2001) to the E

EMBL; AL161574; CAB79697.1;

EMBL; AR013392; BAB09885.1;

EMBL; AY052341; AAK96533.1;

EMBL; AY061910; AAL31237.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Ribosomal protein S30 homolog (40S ribosomal protein S30 homolog)
(At2919750/F6F22.22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamipa A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick J. Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis cDNA clones."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9M0E4
Q9M0E4;
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Mewes H.W., Lemcke K.,
Submitted (MAR-2000) t
                                                                                                                                                                                                                                                                                                                                                    Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Suduen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,367,185
physically assigned Pl and TAC clones.";
DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eddicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kim C.J., Chen H.,
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                                      Local
             . Similarity
22; Conserv
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62 AA;
             Conservative
37.3%; 5-
100.0%; Pr/
0;
                                                                                                                     6887 MW;
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he EMBL/GenBank/DDBJ
                                   Score 22;
Pred. No.
                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
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                                                                                                                   95D8F3EB72F53F33 CRC64;
             Mismatches
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                                      DB 10;
2.4e-16;
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5 bp covered
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             Indels
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Yu S.,
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Best Local
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Ephydroidea; Dros
NCBI_TaxID=7227;
Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. A., Daviens M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Butler M.M., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20, CG15697 protein (RH008962p). CG15697.
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Q15351;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
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SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruehlmann A., Gupta A., Terhorst C.;
"A novel murine RRM-type protein and its human homolog.'
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
EMBL; X75315; CAA53064.1; -.
TITLEGOEGAL DAY
TOTATETC. TERROGEAL DAY
TOTATETC. TERROGEAL
TOTATETC. TERRO
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=THYMUS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000504; RNA_rec_mot.
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Primates;
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100.0%;
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Last annotation update)
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Pred. No
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RN 1218
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Q18231;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Cou Craxton M., Dear S., Du Z., Durbin R., Fayello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnst Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
                                                                                       STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                        Rhabditidae; Pel
NCBI_TaxID=6239;
                                                                                                                                                                                           Caenorhabditis elegans
Eukaryota; Metazoa; Ner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2001) to the EMB Submitted (DEC-2001) to the EMB EMBL; AE003732; AAF55815.1; -- EMBL; AY071683; AAL49305.1; -- E1yBase; FBgn0038834; CG15697. InterPro; IPR000626; Objquitin.
                                                                                                                        SEQUENCE FROM N.
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                                                                                                                                                                                                                                           C26F1.4 protein
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15; Conserv
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                                                                                                                                                                          Peloderinae;
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AA; 14585
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100.0%; Pr
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Last sequence update)
Last annotation update)
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Pred. No.
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Ld. No. 2e-08;
Mismatches
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Park S.,
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Smith H.O.,
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RESULT 11

Q962Q1

ID Q962Q

AC Q962Q

AC Q962Q

DT 01-DE

DT 01-JU

DE RIbos

Spodc

CC Ptery

OC Ptery

OC NOCTU

RN [1]

RP SEQUE

RA Lande

RA Lande

RA Lande

RA Pull

RT Spodc

RT Spodc

RT Spodc

RT SEQUE

RESULT

SQ SEQUE
RESULT 12
Q9S9J0
ID Q9S9J
AC Q9S9J
DT 01-MADT 01-MA
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Q9S9J0;
Q9S9J0;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN BRADE L., Brade Geisel C., Stellyes L., Brade The sequence of C. elegans The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M. Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee Smaldon N., Smith A., Sonnhammer Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
                                                                                                                                                                                                                               Landais I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber Nononr-Cerutti M., Fournier P., Devauchelle G.;
"Full-length ribosomal protein sequence from an EST library Spodoptera frugiperda cells (Sf9).";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400225; AAK92197.1;
                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein S30.
Spodoptera frugiperda (Fall armyworm).
Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000626; Ubiquitin. Pfam; PF00240; ubiquitin; 1. SMART; SM00213; UBQ; 1.
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STRAIN-BRISTOL N2;
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13; Conserv
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llarity 100.0%;
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100.0%; Pr
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Pred. No.
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C26F1.";
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Best Local :
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-APCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Tatusov R.L., Subathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe P., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe P., Doucette-Stamm L., Soucaille P., Daly Patusov R.L., Sabathe P., Doucette-Stamm L., Soucaille P., Daly P., Sabathe P., Daly P., 
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Q971R7;
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AC007230; AAD26867.1; -.
NON_TER 309 309 45E11D7AF877A0D1 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schw
Li J., Kremenetskaia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uncharacterized protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., L. Li J., Kremenetskala I., Ngan I., Luros J., Gonzalez A., Alta Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Hulzar L., Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; "Arabidopsis thaliana chromosome 1 BAC T23K8 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T23K8.1 (Fragment).
                                                                                                                                                                                                                       EMBL; AE007667; AAK79540.1; -.
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                                          KOEKKKKK
  KQEKKKKK 131
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9; Conser
                                                                                      Similarity
8; Conser
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                                                                                         Conservative (
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                                                                                                                                                                               16388 MW;
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Pred. No.
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                                                                                                                                                                               387D5F8D11444E7A CRC64;
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                                                                                  Mismatches
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D. 0.14;
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ez A., Altafi
                                                                                                                                                                                                                                                                                                                                        Daly M.J.,
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RESULT 15
Q9RSE5
ID Q9RSE
AC Q9RSE
AC Q9RSE
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OPIG57

ID 09165

AC 09165

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DT 01-00

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RO HIST

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RN [1]

RP SEQUENT

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Matches 7
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Best Local Similarity
Matches 7; Conserv
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COKEY C., Bakare O.O., Mobley H.
"H-NS is a Repressor of the Prot
Activator Gene ureR.";
J. Bacteriol. 0:0-0(2000).
EMBL; AF240693; AAF61240.1; -.
HSSP; P08936; 1HNR.
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20036896; pubMed=10567266; white O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vi-may-2000 (TrEMBLrel. 13, 01-may-2000 (TrEMBLrel. 13, 01-mar-2002 (TrEMBLrel. 20, Hypothetical protein DR2179, DR2179.
                                                                                                                                                                                                      radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002051; AAF11732.1; -.
TIGR; DR2179; -.
                                                                                                                                        Hypothetical protein; Complete SEQUENCE 154 AA; 16181 MW;
                                                                                                                                                                                                                                                                                                                          "Genome sequence of the radioresistant bacterium radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-R1
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Q9L657;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                     Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcaceae;
NCBI_TaxID=1299;
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01-MAY-2000
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Pfam; PF00816; Histone_HNS; 1.
ProDom; PD007337; Histone_HNS; 1.
SMART; SM00528; HNS; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Histone-like nucleoid structuring protein.
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                                            Similarity
             Conservative
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                                         11.9%;
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          0;
                                  Score 7; D; Pred. No.
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Pred. No.
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58AA86884AA0D4C4 CRC64;
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      Mismatches
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                                     DB 16;
o. 11;
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RESULT 17
Q9ZQB1
ID Q9ZQB
AC Q9ZQB
DT 01-MA
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                                                                                                                                                                               STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito I
Carrera A.J., Creasy T.H., Bell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006282; AAD20137.2;
EMBL; AC006282; AAD20137.2;
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 173 AA; 20478 MW; 57A67DCDA47E75FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0970B1;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
Putative DNA binding protein with ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NBB4;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Stretchin-MLCK (Fragment).
STRN-MLCK OR CG8304 OR CG18255.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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157 AA;
         Conservative
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n with homeobox domain.
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a Novel M
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Member of the Titin/Myosin Light
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InterPro; IPRO01882; Biotin_attach.
InterPro; IPR001882; Biotin_lipoy1.
InterPro; IPR000089; Biotin_lipoy1.
InterPro; IPR00364; biotin_lipoy1; 1.
IPRINTS; PR01071; ACCOABIOTINCC.
TIGRPAMS; TIGR00531; BCCP; 1.
PROSITE; PS00188; BIOTIN; UNKNOWN_1.
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Q64075;
01-NOV-1996 (TrEMBLrel. 0:
01-NOV-1996 (TrEMBLrel. 0:
01-DEC-2001 (TrEMBLrel. 1:
Nucleoporin p62 homolog p:
                                                                                                                                                                                                            Wang 2.Q., Akmal K.M., Kim K.H.;
"An unusual nucleoporin-related messenger ribonucleic in the germ cells of rat testis.";
Biol. Reprod. 51:1022-1030(1994).
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and sequence of the aroD gene of Brucella abortus."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP326476; AAK27449.1; -. HSSP; P02905; 3BDO.
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01-JUN-2001
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                                                                                                                                SEQUENCE
                                                                                                                                                                                            Biol. Reprod. 51:1022-1030
EMBL; S75997; AAB33384.1;
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Sciurognathi;
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Sequence features of the region
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP001297; BAB03010.1; -.
SEQUENCE 224 AA; 26999 MW;
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O9FZ76;
01-MAR-2001 (TIEMBLIEL 1
01-MAR-2001 (TIEMBLIEL 1
01-MAR-2002 (TIEMBLIEL 2
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O9LIR5;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 3, BAC clone:F14013.
Genomic DNA, chromosome 3, BAC clone:F14013.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
                                                                                                                                                                               Federsgiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.

Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core et

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Kaneko T., Kato T.
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16, Last sequence update)
20, Last annotation update)
protein L6 (Putative 60S ribosomal protein
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RY SEALUNCY. COLLUMBIA;

RX MEDLINE=21016719; PubMed=11130712;

RX MEDLINE=21016719; PubMed=1130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Chung M.K., Conn L., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hopper S., Lee A., Leu J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Militscher J., Miranda M., Nigyyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nigyyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Torlumi M.J., Town C.D.,

RA Sun H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
                          RESULT OPECATION OF THE PROPERTY OF THE PROPER
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Q9C9C6;
O1-JUN-2001 (TrembLrel. 17, C:
O1-JUN-2001 (TrembLrel. 17, L:
O1-MAR-2002 (TrembLrel. 20, L:
O1-MAR-2003 (TrembLrel. 20, L:
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EMBL; AV026238; AAF98420.1; -.
EMBL; AV072496; AAK96861.; -.
EMBL; AV072496; AAK968611; -.
EMBL; AV072496; AAK968611.; -.
EMBL; AV072496; AAK968611.; -.
EMBL; AV072496; AAK968611.; -.
EMBL; AV072496; AAK968611.; -.
EMBL; AV072496; AAL66911.1; -.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Haysshizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.x., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pfam; PF01159; Ribosomal_L6e; 1.
ProDom; PD009812; Ribosomal_L6E; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein L6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis R.W.;
the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1ED96BB26A0F85CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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RP SEQUENCE FROM COLUMBIA;

RX MEDLINE-21016719; PubMed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H.,

RA Cill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jekins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

"Samuence and analysis of chromosome l of the plant Arabidopsis
             RESULT OPPOSITE AND ACT OF ACT OPPOSITE ACT 
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Best Local S
Matches 7
                                                                                                                          Nguyen M., I
Nguyen M., Karlin Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                            Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Ski M., Shinn P., Yamada K., Shinozaki K., Scker J., Theologis A., Davis R.W.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat)
Putative 60s ribosomal protein L6.
F2P9.8 OR ATIG74050.
Real-Marketing (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9C9C5 PRELIMINARY;
Q9C9C5;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000915; Ribosomal_L6E.
Pfam; PF01159; Ribosomal_L6e; 1.
ProDom; PD009612; Ribosomal_L6E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ecker J., Theologis A., Dav. Submitted (NOV-2001) to the EMBL; AC016662; AAG52524.1; EMBL; AY062622; AAL32700.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKKKKKT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              837890EFAB082A40 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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RESULT 25
Q9NSX
ID Q9NSX
AC Q9NSX
AC Q9NSX
OT 01-OC
DT 01-OC
DT 01-OC
DT 01-OC
DE Hypot
GN DKF2P
GN DKF2P
GN Homo
OC Eukar
OC Mamma
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conser
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EMBL; AC016662; AAC52527.1; -.
EMBL; AY054573; AAK56764.1; -.
EMBL; AY081305; AAL91194.1; -.
Interpro; IPR000915; Ribosomal_L6E.
Pfam; PF01159; Ribosomal_L6E; 1.
ProDom; PD009512; Ribosomal_L6E; 1.
                                Q9NSK3 PRELIMINARY; PRT; 283 AA.
Q9NSK3;
Q9NSK3;
O1-OCT-2000 (TremBLrel. 15, Created)
O1-OCT-2000 (TremBLrel. 15, Last sequence update)
O1-OCT-2000 (TremBLrel. 15, Last annotation update)
Hypothetical 31.4 kDa protein (Fragment).
DKFZP762I166.......
                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL590463; CAC36648.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 259 AA; 28708 MW; 357BF1A6821CFE5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Seeger K., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9AD23; PRELIMINARY;
Q9AD23;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor. Plasmid SCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein SCP1.127. SCP1.127.
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                          Ropwood D.A.;
                                                                                                                                                                                                             127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                        G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKKKKKT 172
                                                                                                                                                                                                             SLARAGK 133
                                                                                                                                                                                                                                        SLARAGK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AA;
                                                                                                                                                                                                                                                                    11.9%; Score 7; DB: llarity 100.0%; Pred. No. 18 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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. 18;
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. 16;
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Best Local S
Matches 7
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Best Local S
Matches 7
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Q95T41;
Q1-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
GH23743p.
CG3441)
                                                                                                                                                                                                                             066535;
01-AUG-1998
01-AUG-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Mirada A., Mungali C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ANG60340; AAL25379.1; -. FlyBase; FBgn0035092; CG3441. SEQUENCE 309 AA; 34197 MW; 620BB8A464BEF487 CRC64;
                                                                                                              Aquifex aeolicus.
Bacteria; Aquificae;
NCBI_TaxID=63363;
                                                                                                                                                                                Riboflavin kinase.
RIBF OR AQ_139.
                                                                                                                                                                                                                                                                                                                         066535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etarygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-MELANOMA;
MEDLINE-98196666; PubMed-9537320; Deckert G., Warren P.V., Gaaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                        153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 GSLARAG 242
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7; Conserv
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7; Conservative 0;
                                                                                                                                                                                                                           3 (TrEMBLrel.
8 (TrEMBLrel.
2 (TrEMBLrel.
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                      N.A.
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21,
    Gaasterland
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Last sequence update)
Last annotation update)
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Pred. No.
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    Lenox A.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 392:353-358(1998).
EMBL; AE000675; AAC06488.1; -.
InterPro; IPR002606; FAD_Synth.
Pfam; PF01687; FAD_Synth; 1.
ProDom; PD003662; FAD_Synth; 1.
TIGRFAMS; TIGR00083; ribF; 1.
Complete proteome.
SEQUENCE 314 AA; 36660 MW; 81
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Q96GN4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Direct Submission.";
Submitted (NOV-2001) to the
EMBL; AC084197; AAL00874.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The sequence of C. elegans cosmid Y73B6BL."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Pfam; PF00892; DUF6; 1.
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                                                                                                                                                                                                                                                                                                         7; Conserv
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA George R.A., Lewis S.E., Richards J., Sahburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards J., Champe M., Pfelffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Denos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Denos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., McPherson D.,
RA Hostin A. No McPherson D., McPherson D.,
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RA Hostin A.
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Matches 7
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Q9W0W6;
01-MAY-2000
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CG3441 prote
CG3441
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Submitted (JUN-2001) to the EMBL/Ge
EMBL; BC00953; AAH09353.1; -.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to kinesin family member 5B.
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 380 AA; 43059 MW; 912B4E7371C23650 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-B-CELL;
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Walliams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhung G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosopphila melanogaster.";
REL Science 287:2185-2195(2000).
REL SCIENCE SEW., AAR47313.1;
RD REMBL; AE003466; AAR47313.1;
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Best Local
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                                 O9S2FO, PRELIMINARY; PRT;
O9S2FO;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequ
O1-JUN-2002 (TrEMBLrel. 21, Last and
Putative ABC transporter ATP-binding
SCO2931 OR SCE19A.31
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            Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                          osteomalacia and uremia.";
Proc. Assoc. Am. Physicians 107:296-305(1995).
EMBL: U28831; AAB02177.1; -.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-96187433; PubMed-8608414;
Kumar R., Haugen J.D., Wieben E.D., Londowski J.M.,
"Inhibitors of renal epithelial phosphate transport
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
   Actinomycetales;
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Actinobacteria; Actinobacteridae; ptomycineae; Streptomyces.
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Q9X4J1;
01-NOV-1999
01-NOV-1999
01-JUN-2002
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the coelicolor A3(2).";
Nature 417:141-147(2002).
-1 SIMILARITY: BELLONGS TO THE ABEMBL; AL096852; CAB51012.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR000644; CBS_domain.
Pfam; PF00005; ABC_tran; 1.
Pfam; PF00571; CBS; 2.
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                                   Actinomycetales;
NCBI_TaxID=1902;
                                                                             Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                   ProVL.
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PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport.
   SEQUENCE FROM N.A.
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SMART; SM00382; AAA; 1.
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James K.D., P.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                               328
                                                                                                                                                                                                                                                                                                                                                                   4 GSLARAG
                                                                                                                                                                                                                                                                                                                               GSLARAG
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 AA;
                                                                                                                                                     (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 21,
                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                               334
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                                                         Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 7; DB
100.0%; Pred. No. 29
Live 0; Mismatches
                                                                           Actinobacteria;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                 PRT;
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                                                         Streptomycetaceae;
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                                                                                                                                                                                                                                 429
                                                                             Actinobacteridae;
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5. 29;
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RESULT 35
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Q91290
Q91290;
01-NOV-1996
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01-0CT-2000
01-0CT-2000
01-JUN-2002
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Replicative DNA helicase. DNAC OR BH4029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000006; ABC_transportr; SMART; SM00382; AAA; 1.
TIGRFAMs; TIGR01186; proV; 1.
PROSITE; PS00211; ABC_TRANSPORTER; ATP-binding; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001198; DnaB_hel.
Pfam; PF00772; DnaB; 1.
TIGRFAMS; TIGR00665; DnaB; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP001520; BAB07748.1; HSSP; P03005; LJWE.
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nalodurans Res. 28:4317-4331(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-86665;
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281 GSLARAG 287
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nilarity 100.0%;
Conservative 0
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(TrEMBLrel.
                                         PRELIMINARY;
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Pred. No.
                                         PRT;
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                                                                                                                                                                                                                                                                                                  D9D6DE17A52EAD3A CRC64;
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Best Local S
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01-OCT-2000 (
01-OCT-2000 (
01-MAR-2002 (
                                                                                                                                                   PROSITE; PSO0411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Microtubules; Motor prote NON_TER 576
SEQUENCE 576 AA; 64518 MW; A21BBE950F4946D6 CRC
                                                                                                                                                                                                                                                                                                                           Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00059; BAA90916.1; -.
HSSP; P17119; 3KAR.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ20052 fis, clone COL00777 (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                               PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NXU4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001404; Hsp90. Pfam; PF00183; HSP90; 1. NON_TER 1 1 SEQUENCE 542 AA; 63096 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amphibian oocyte.";
Dev. Biol. 168:247-258(1995).
EMBL; L32987; AAA92343.1; -.
HSSP; P07900; IYER.
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MEDLINE=95246904; PubMed=7729567;
Commailleau P., Billoud B., Sourrouille P., Moreau N., Angelier N.;
Pevidence for a 90 kDa heat-shock protein gene expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pleurodeles waltlii (Iberian ribbed newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Heat shock protein 90 (Fragment).
HSC90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pleurodeles.
NCBI_TaxID=8319;
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  22 QEKKKKK 28
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                                                      Similarity 7; Conserv
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                                                        Conservative
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100.0%; Pr
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Primates;
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Pred. No.
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                                                                                                                                                        A21BBE950F4946D6 CRC64;
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D. 37;
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EMBL; AP003005; BAB51602.1; ...

InterPro; IPR003594; ArPbind_ATPase.

InterPro; IPR003594; Bact_sens_pr_C.

InterPro; IPR004358; Bact_sens_pr_C.

InterPro; IPR003660; HAMP.

InterPro; IPR003661; HIS_KIN_sig.

Pfam; PF00572; HAMP; 1.

Pfam; PF00518; HATPase_C; 1.

PRINTS; PR00344; BCTRLSENSOR.

SMART; SM00308; HAMP; 1.

SMART; SM00388; HATPASSE_C; 1.

SMART; SM00388; HATPASSE_C; 1.
                                                                                                                                                                                                                                                                                                                                    09M8T5;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
F13E7.12 protein.
F13E7.12.
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Be
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Arabidopsis thaliana chromosome III BAC F13E7 genor
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databt
EMBL; AC018363; AAF26966.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinase; C
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Watanabe A., Idesawa K., Ishkawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbioti Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
Two-component sensor histidine kinase, ExoS.
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01-OCT-2001
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                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 SLARAGK 511
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7; Conserve
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E 594 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 65169
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                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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o. 40;
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                                                 genomic sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T., Sasamoto ., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  symbiotic bacterium
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RESULT Q9WC26

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Best Local 9
                                              Matches
                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                       InterPro; IPRO01611; LRR.
InterPro; IPRO01592; LRR.out.
InterPro; IPRO02290; Ser_thr_pkinase.
InterPro; IPRO02290; Ser_thr_pkinase.
InterPro; IPRO04040, STY_pkinase.
InterPro; IPRO01245; TYr_pkinase.
InterPro; IPRO01537; Herpes_glycop_D; 1.
Pfam; PPO0565; LRR; 2.
Pfam; PPO0069; pkinase; 1.
PRINTS; PRO0109; TYRKINASE.
IPRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00370; LRR; 2.
SMART; SM00370; LRR; 2.
SMART; SM00221; STYKG; 1.
PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00118; PROTEIN_KINASE_ST; 1.
PROSITE; PS00118; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9MOD8 PRELIMINARY; PRT; 863 AA.

O9MOD8;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Serine/threonine-specific receptor protein kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000875; Cecropin.
InterPro; IPR00053; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
PROSITE; PS00258; CECROPIN; UNKNC
SEQUENCE 806 AA; 91859 MW; AF
                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                           Transferase
SEQUENCE |
                                                                                                                  ATP-binding; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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QEKKKKK 510
                    QEKKKKK
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                                            Similarity 100
7; Conservative
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100.08; P1
                                                                                           96557
                                                                                                                  Receptor;
                                                         11.9%;
                                                                                           MW;
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                                                         Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNKNOWN_1.
W; AFE6F9AED5D4BBFD
                                              0
                                                                                                                  Serine/threonine-protein
                                                                                           32AE253F9C708427
                                               Mismatches
                                                         No.
                                                        DB 10;
o. 57;
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OF PROTEIN KINASES
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                                                                    Length 863
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                                                                                           CRC64;
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Matches
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InterPro; IPR002548; Alpha_E1_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR000936; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha_E1_glycop; 1.
Pfam; PF001589; Alpha_E2_glycop; 1.
Pfam; PF00943; Alpha_E2_glycop; 1.
Pfam; PF00943; Alpha_E3_glycop; 1.
Pfam; PF00943; Alpha_E3_glycop; 1.
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                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=98347778; Pubmed=9684636;

Oberste M.S., Fraire M., Navarro R., Zepeda C., Zarate M.L.,

Ludwig G.V., Kondig J.F., Weaver S.C., Smith J.F., Rico-Hesse J

"Association of Venezuelan equine encephalitis virus subtype II
"Association of Venezuelan equine encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MENA II;
STRAIN-MENA II;
STRAIN-MENA II;
MEDLINE-99101297; PubMed-9886206;
Kinney R. M., Pfeffer M., Tsuchlya K.R., Chang G.J., Roehrig J.T.
"Nucleottde sequences of the 26S mRNAs of the viruses defining
"Nucleottde sequences of the 26S mRNAs of the viruses defining
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"Nucleottde sequences of the 25S mRNAs of the viruses defining the viru
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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two
[2]
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Venezuelan equine encephalitis virus.
Viruses, ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9YKD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polyprotein.
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7; Conserv
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llarity 100.0%;
Conservative
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8; TOGAVIRIN
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POLYPROTEIN CLEAVAGE PRODUCT E3
ENVELOPE GLYCOPROTEIN 2.
6K POLYPROTEIN CLEAVAGE PRODUCT
ENVELOPE GLYCOPROTEIN 1.
MW; 0E3321D41F4DEE39 CRC64;
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Best Local S
Matches 7
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Best Local S
Matches 7
                                                                Virology 219:314-320(1996).

EMBL; U34999; AAB04683.1; -.

HSSP; P03315; 1VCP.

InterPro; IPR001836; Alpha_E1_glycop.
InterPro; IPR002548; Alpha_E2_glycop.
InterPro; IPR00936; Alpha_E2_glycop.
InterPro; IPR00939; Togavirin.

Pfam; PF00944; Alpha_Core; 1.

Pfam; PF00944; Alpha_E1_glycop; 1.

Pfam; PF00943; Alpha_E2_glycop; 1.

Pfam; PF00943; Alpha_E2_glycop; 1.

Pfam; PF01563; Alpha_E3_glycop; 1.

PRINTS; PR00798; TOGAVIRIN.
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Q88979;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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InterPro;
InterPro;
                                                       Polyprotein.
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Venezuelan equine encephalitis virus.
Viruses; ssRNA positive-strand viruses,
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J. Virol. 76:1718-1730(2002).
EMBL; U96408; AAD19216.1; -.
EMBL; AF448538; AAL47153.1; -.
                                                                                                                                                                                                                                       Oberste M.S., "Complete sequ
                                                                                                                                                                                                                    nsP3.";
                                                                                                                                                                                                                             "Complete sequence of reveals conserved and
                                                                                                                                                                                                                                                              MEDLINE=96204604; PubMed=8623548;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Alphavirus.
NCBI_TaxID=11036;
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InterPro;
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Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., W
"Positively charged amino acid substitutions in the
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STRAIN-OAX142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erPro; IPR001836; Alpha_core.
erPro; IPR002548; Alpha_El_glycop.
erPro; IPR002536; Alpha_E2_glycop.
erPro; IPR002533; Alpha_E3_glycop.
erPro; IPR000930; Togavirin.
m; PP00944; Alpha_core; 1.
m; PP01589; Alpha_E2_glycop; 1.
m; PP00943; Alpha_E2_glycop; 1.
m; PP00943; Alpha_E3_glycop; 1.
m; PP00943; Alpha_E3_glycop; 1.
m; PP01563; Alpha_E3_glycop; 1.
m; PP01563; Alpha_E3_glycop; 1.
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 larity 100.0%;
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uence of Venezuelan equine encephalitis virus
rved and hypervariable domains within the C te
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Matches 7
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O8V291;

O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence

O1-JUN-2002 (TrEMBLrel. 21, Last annotatic

Structural polyprotein.

Venezuelan equine encephalitis virus.

Viruses; ssRNA positive-strand viruses, no
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J. Virol. 76:1718-1730(2002).
EMBL; AF448537; AAL47151.1; -.
InterPro; IPR001836; Alpha_E2_glycop.
InterPro; IPR0002548; Alpha_E2_glycop.
InterPro; IPR000936; Alpha_E2_glycop.
InterPro; IPR000933; Alpha_E3_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha_Core; 1.
Pfam; PF00944; Alpha_E1_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
Pfam; PF01563; Alpha_E3_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alphavirus.
NCBI_TaxID=11036;
[1]
                              SEQUENCE FROM N.A.
STRAIN-80076;
MEDLINE-21657447; PubMed-11799167;
MEDLINE-21657447; PubMed-11799167;
Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
"Positively charged amino acid substitutions in the E2 envelope glycoprotein are associated with the emergence of venezuelan equencephalitis virus.";
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Venezuelan equine encephalitis virus.
Viruses; ssRNA positive-strand viruses, no alphavirus.
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SEQUENCE 1254 AA;
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SEQUENCE 1264 AA;
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Venezuelan equine encephalitis virus.
Viruses; ssRNA positive-strand viruses,
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGFAUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPATION:
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                         ATTORNEY/AGENT INFORMATION:
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LENGTH: 409 amino acids
TYPE: amino acid
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NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP195-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 KQEKKKK 366
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP:
                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                            CITY: Lexington
                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02173
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Tao, Jianshi
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Gallant, Paul L.
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Pred. No.
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APPLICANT: ZIRLE, ROSS
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
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US-09-568-102-5
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Best Local Similarity
7; Conserv
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09568102 Patent No. 6346404
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
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Zirkle, Ross
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; SEQ ID NO 5; LENGTH: 7257; TYPE: PRT; ORGANISM: Sorangium cellulosum US-09-567-969-5
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Best Local Similarity
Thes 7; Conserv
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                                ; SEQ ID NO 5; LENGTH: 7257; TYPE: PRT; ORGANISM: Sorangium cellulosum US-09-568-480-5
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Best Local
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   Query Match
                                                                                                             CURRENT APPLICATION NUMBER: US/09/568,480 CURRENT FILING DATE: 2000-05-10 PRIOR APPLICATION NUMBER: 09/335,409 PRIOR FILING DATE: 1999-06-17 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                 APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cyr, Devon
APPLICANT: Goetlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvar
APPLICANT: Zirkle, Ross
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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Zirkle, Ross
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   11.9%;
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   Score 7;
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   DB 4;
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Length 7257;
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                                                                                             ; SEQ ID NO 5;
LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-472-5
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US-09-568-472-5
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Best Local
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                                                                                                                                                                         APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30502A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR PETLING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.0
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,486
CÜRRENT FILING DATE: 2000-05-10
CÜRENT FILING DATE: 2000-05-10
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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PRIOR FILING DATE: 1999-06-17
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Zirkle, Ross
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                              11.9%; Score 7; DB ilarity 100.0%; Pred. No. 95 Conservative 0; Mismatches
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100.0%; Prr
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); Mismatches
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                                               DB 4;
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                                                                Length 7257;
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7250 SLARAGK 7256

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Query Match
Best Local Similarity
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                                                                                 US-09-082-358B-62
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; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-899-5
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US-09-567-899-5
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/09082358B
Patent No. 6469153
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
APPLICANT: Li, Xingquiang
TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
TITLE OF INVENTION: EIP-1, and EIP-3
FILE REFERENCE: 0575/54804
CURRENT APPLICATION NUMBER: US/09/082,358B
CURRENT FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 24
                                   GENERAL INFORMATION:
                                                   Sequence 62, Application US/09082358B Patent No. 6469153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
SEQ ID NO 5
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APPLICANT: Goff, Stephen P. APPLICANT: Li, Xingquiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goerlach, Joern TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istva
APPLICANT: Zirkle, Ross
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                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: murine
                                                                                                                                                                                                                                                                                                                           LENGTH:
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Zirkle, Ross
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Pred. No.
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US-08-851-843A-201
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Best Local Similarity
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LENGTH: 15
TYPE: PRT
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INFORMATION FOR SEQ ID NO:
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CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS, TITLE OF INVENTION: EIP-1, and EIP-3 FILE REFERENCE: 0575/54804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: murine
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/846,017
                             TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 06-MAY-1997
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                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
STATE: California
                                                                                                                                  CLASSIFICATION:
                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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T: Andrews, William H.
INVENTION: No. 6093809el Telomerase
F SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08851843A
               (415)
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Morin, Gregg B.
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                                                                                                                                                01-OCT-1996
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            576-0300
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                                                                                                                                                                US 08/724,643
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                                                                                                                                                                        APPLICATION NUMBER: US 01 FILING DATE: 09-MAY-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                           APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 PRIOR APPLICATION DATA:
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                               FILING DATE: 14-AUG-1997
PRIOR APPLICATION UNBER: US 08/915 507
FILING DATE: US 08/915 507
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APPLICATION NUMBER:
FILING DATE: 18-APR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 01-OCT-1996
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Similarity 100.0%;
6; Conservative
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ENTION: Human Telomerase Catalytic Subunit
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18-APR-1997
MBER: WO PCT/US97/17618
01-OCT-1997
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b; Pred. No. 7.2
0; Mismatches
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Best Local Similarity
watches 6; Conserve
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                                                                                                                                                                                       SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 06-MAY-1997
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                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF IN
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
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                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
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VENTION: No. 6261836el Telomerase
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Chapman, Karen B.
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                                                               18-APR-1997
JMBER: US 08/724,643
01-OCT-1996
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                                                                            US 08/844,419
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REGISTION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: 11
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les 6; Conserv
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPle, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
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FILING DATE: 29-Oct-1999
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
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TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                          APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
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Harley, Calvin
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Nakamura, Toru
Chapman, Karen B.
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RESULT 18
US-09-227-357-479
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-09-430-323-201
                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: The Regents of the University of California TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit TITLE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 189
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
                                                                                                                                                                                                                Sequence 479, Application US/09227357 Patent No. 6342581
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Matches
                                                                                                                                  APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
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                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                   48 TFGKKK 53
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STRANDEDNESS: <Unknown>
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100.0%; Pr
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100.08; F1
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s; Pred. No. 12;
0; Mismatches
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b; Pred. No. 7.2
0; Mismatches
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APPLICATION NUMBER: 60/051,925

1997-07-08

APPLICATION NUMBER: 60/051,929 FILING DATE: 1997-07-08

APPLICATION NUMBER: 60/052,803

1997-07-08

APPLICATION NUMBER: 60/051,931 FILING DATE: 1997-07-08

APPLICATION NUMBER:

60/052,732

FILING DATE: 1997-07-08

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EARLIER APPLICATION NUMBER: 60/UDA;

EARLIER FILING DATE: 1997-07-08

TABLE FOR TOWN NUMBER: 60/05

TABLE TOWN NUMBER: 60/05
                                                                                           ; ORGANISM: Homo sapiens US-09-227-357-479
                                                                                                                       NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 479
LENGTH: 51
TYPE: PRT
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EARLIER
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 23 EKKKKK 28
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FILING DATE: 1997-09-12
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                                Conservative
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                              10.2%; Score 6; DB 4
100.0%; Pred. No. 19;
tive 0; Mismatches
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                                              DB 4;
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Query Match
Best Local Similarity
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US-08-569-749-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino Types
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Patent No. 6187557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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CITY: S
STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                             STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
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CLASSIFICATION: 514
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ZIP: 94111
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                                                                COUNTRY:
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linear
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                                                                                                                               HOHBACH, TEST, ALBRITTON & HERBERT
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PCT-US96-12860-5
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                                                                                                        TELEFAX: (415)398-324 INFORMATION FOR SEQ ID NO:
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NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA PAPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
                                                                                                                                                                                                                          CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
              MOLECULE TYPE:
                                                                                                                                     TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: IN NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BrEZNEY, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-1
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LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                           STRANDEDNESS:
TOPOLOGY: 11
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SOFTWARE: Patentl
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linear
                            linear
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PatentIn Release #1.0, Version #1.30
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                                        single
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100.0%; Pr
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RESULT 23
US-09-082-358B-43
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                                                                                                            GENERAL INFORMATION:
                                                                                                                            Sequence 43, Application US/09082358B Patent No. 6469153
                                                                                                                                                                                                                                                                                       Matches
                             APPLICANT: Goff, Stephen P.
APPLICANT: Li, Xingquiang
TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
TITLE OF INVENTION: EIP-1, and EIP-3
FILE REFERENCE: 0575/54804
                                                                                                                                                                                                                                                                                                                     Query Match
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GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/082,358B CURRENT FILING DATE: 1998-05-20
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Best Local (
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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APPLICATION NUMBER:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: FLEHR, HOHBACH, TE:
STREET: 4 Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/12860 FILING DATE: 06 AUG 1996
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RESULT 25
US-08-511-485-18
; Sequence 18, Application US/08511485
; Patent No. 5919912
                                                                                                                                Query Match
Best Local Similarity
"---hes 6; Conserv
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                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-971-089-2
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US-08-971-089-2
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Patent No. 6376174
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APPLICANT: Pulst, Stefan M.
                                                                                                                                                                                                                                                                                      TELEFAX: (619)535-8949
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TYPE: PRT
ORGANISM: murine
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ramos, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Scoles, Daniel R.
TITLE OF INVENTION: NUCLEIC ACID ENCODING
TITLE OF INVENTION: SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERETO
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4370 La
CITY: San Diego
STATE: Californi
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                                                                                        15 EKKKKK 20
                                                                                                                 23 EKKKKK 28
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                      (619)535-8949
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                                                                                                                                                 Conservative
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                                                                                                                                                           10.2%;
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                                                                                                                                                                                                                                                                                                                                Patent No. 5919912
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    Sequence 19,
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/511
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 68 amino a TYPE: amino acid STRANDEDNESS: not TOPOLOGY: both MOLECULE TYPE: prot
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ric
STREET: 225 Franklin
                                                                                                                                                                                                                                                                              APPLICANT: Korneluk, Robert G. APPLICANT: Mackenzie, Alexander E. APPLICANT: Baird, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             TITLE OF INVENTION:
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STATE: MA
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                                                                                                                                                          CITY: Boston
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5919912
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100.0%; Pre
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lin Street
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Query Match
Best Local Similarity
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US-09-091-725-51
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                                                                                                                                    APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. VICTOR Donahue
REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
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Patent No. 6329141
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Matches 6; Conserv
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                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Im
TITLE OF INVENTION: an
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
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MEDIUM TYPE: Floppy disk
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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NAME: Clark, Paul T.
RECISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
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21 SLARAG 26
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TELEFAX: 200154
                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/091,725 FILING DATE: 23-DEC-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United ZIP: 20006-1888
                                                                                                            TOPOLOGY:
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                                                                                                                       amino acid
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              Conservative
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      10.2%; Scc.
100.0%; Pr
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            Score 6; DB 4; ; Pred. No. 43; 0; Mismatches
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Pred. No.
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            Gaps
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           CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
PRIOR FILING DATE: 1997-06-09
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; STRANDEDNESS:
; TOPOLOGY: LIN
; MOLECULE TYPE:
US-08-871-732A-1
Sequence 1, Application US/09346510B
Patent No. 6281014
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Wang, Yinxiang
TITLE OF INVENTION: SH3-Containing
FILE REFERENCE: D6221CIP
                                                                                                                     US-09-346-510B-1
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US-08-871-732A-1
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-682-1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: MCGREGOR, MARTIN L
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKETTE 3.5 INCH 1.44 MB STORAGE
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: O'BRII APPLICANT: WANG,
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MYDE: SIN
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les 6; Conserv
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5380 WEST 34TH STREET, #345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'BRIEN, TIMOTHY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                              LINEAR
                                                                                                                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                                                                              SINGLE
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                   SH3-Containing Protein,
                                                                                                                                                                                                                                                          10.2%; So
100.0%; F
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,329
                                                                                                                                                                                                                                                          %; Score 6; DB 4
%; Pred. No. 46;
0; Mismatches
                                                                                                                                                                                                                                                                          DB 4;
                     DNA and Uses Thereof
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                                                                                                                                                                                                                                                                                          Length 154;
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RESULT 31
US-09-183-861-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-533-669A-4
          Sequence 4, Application US/09183861 Patent No. 6365165 GENERAL INFORMATION:
                                                                                                                                                                                          Query Match
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Best Local
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                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Corixa
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/00
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                           160 AKRRMQ
                                                                                                                                                               Local Similarity
nes 6; Conserv
                                                                                                                                    32 AKRRMQ 37
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mes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J. REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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GY: linear
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VENTION: LEISHMANIA ANTIGENS FOR USE IN THE
VENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                           165
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                                                                                                                                                               Conservative
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Reed, Steven G.
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Pred. No.
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Pred. No.
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51;
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5. 46;
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RESULT 32
US-09-022-765-4
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      APPLICANT: Dillon, Davin C. APPLICANT: Skeiky, Yasir A.W. TITLE OF INVENTION: LEISHMAN
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TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                APPLICANT: Reed, Stever APPLICANT: Campos-Neto,
                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                   APPLICANT:
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                                                                                            STREET: 6300 CONTY: Seattle STATE: Washing
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                            COUNTRY:
                                                                                                                                        ADDRESSEE:
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Skeiky, Yasir A.W.
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                                                                                                                                                                                                                                                                Reed, Steven
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100.0%; Pr
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Pred. No.
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                                                                                                                           701 Fifth Avenue
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51;
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PatentIn Release #1.0,

Version #1.30

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43
TELECOMMUNICATION INFORMATION:
TOT FORMOMENT
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NAME: Maki, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELEPIONE: (206) 622-4900
TELEPIAX: (206) 682-6031
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                                                                                                                                 TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 175 amino acids
                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR XA
TITLE OF INVENTION: INHIBITORY ACTIVITY
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APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
              MOLECULE TYPE:
HYPOTHETICAL:
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ANTI-SENSE:
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                                                              TYPE: amino acid
STRANDEDNESS: si
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                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                               linear
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            : protein
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                                                              single
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Best Local Similarity
Watches 6; Conserve
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; LOCATION:
US-08-468-347-24
                                                                                            ; LOCATION: US-08-467-389-24
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US-08-467-389-24
                                    Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                          TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 03:
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 08-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal FEATURE:
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                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acid
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ADDRESSEE: Cooper & Dunham
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR XA
                                                                                                                                    FEATURE:
                                                                                                                                                                                       TOPOLOGY: li
                                                                                                                                              RAGMENT TYPE:
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24 KKKKKT 29
                                    Local Similarity
les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10112
                                                                                                                                                                                                                                 amino acid
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                                                 10.2%; Score 6;
100.0%; Pred. N
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Pred. No. 56;
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                                    red. No. 56
Mismatches
                                                   DB 2
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191 KKKKKT 196

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RESULT 36
US-08-469-219-24
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                                                                                                                            Sequence 24, Application US/08469219 Patent No. 5863534
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Patent No. 5858970
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
SEQUENCE TENGTH: 197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/225,44
ETILING DATE: 08 APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,977-9550
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                                                                                                              GENERAL INFORMATION:
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MOLECULE TYPE: Pro-
HYPOTHETICAL: NO
HYPOTHETICAL: NO
                                      APPLICANT: Werber, I
APPLICANT: Levanon,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                          24 KKKKKT 29
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STRANDEDNESS: sir
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STATE: New York
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USA
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Pred. No.
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RESULT 37
US-09-228-152-24
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; LOCATION:
US-08-469-219-24
US-09-228-152-24
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY
FILE REFERENCE: 43020aya
                                                                                                                       CURRENT APPLICATION NUMBER: US/09/228,152
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/09228152 Patent No. 6211341
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INFORMATION FOR SEQ ID NO:
                                                               LENGTH: 197
TYPE: PRT
ORGANISM: Artificial Sequence
               OTHER INFORMATION: Description of Artificial Sequence: Deduced amino OTHER INFORMATION: acid sequence of clone pSP65-XaI-13.
                                                        FEATURE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CITY: New 1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les 6; Conserva
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STRANDEDNESS: single
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30 Rockefeller Plaza
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1..197
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tive 0; Mismatc
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Sequence 3, Application
Patent No. 6232440
GENERAL INFORMATION:
APPLICANT: Hillman,
                                                                                   US-09-295-055-3
                                                                                                  RESULT 39
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Best Local Similarity
Matches 6; Conser
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Patent No. 5932712
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,801
FILING DATE: Herewith
APPLICANT: Hillman, Jennif APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REGISTRATION NUMBER: PF. TELECOMMUNICATION INFORMATION: TELEPHONE: 415.855-555
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
NUMBER OF SEQUENCES: 3
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                                                                                                                                                    217 KKKKKT 222
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                Application US/09295055
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                                                                                                                                                                                                                                                                                                                                                                                             234 amino acids
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Corley, Neil C.
Shah, Purvi
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100.0%; Pred. No
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Pred. No. 56;
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                                                                            CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                             RESULT 40
US-09-149-476-568
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Best Local S
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                                               EARLIER APPLICATION NUMBER: 60/040,626 EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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TONE: 1514949
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               APPLICATION NUMBER: 60/040,334 FILING DATE: 1997-03-07
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NUMBER: 60/040,336
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APPLICATION NUMBER: 60/043,670

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SEQ ID NO 20
LENGTH: 316
TYPE: PRT
ORGANISM: Glycine max
US-09-347-803-20
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Best Local Similarity
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                                                                                                                                                                                                                               APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-347-803-20
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                               2 VHGSLA 7
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ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,862
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,887
ER FILLING DATE: 1997-08-22
ER FILLING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
FILING DATE: 1997-08-22
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APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
RESULT 44
US-08-729-214-27
: Sequence 27, Application US/08729214
; Patent No. 5817502
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; SEQ ID NO 16
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-803-16
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US-09-347-803-16
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US-09-615-192A-389
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 389
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APPLICANT: Bloksberg, Leonard
APPLICANT: Havukkala, Ilka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U
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TYPE: PRT
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GENERAL INFORMATION:

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; MOLECULE TYPE: protein US-08-729-214-27
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US-09-028-934-27
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Best Local :
                                                                                                                                                                                                                                                                                                                     Patent No. 6117670
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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INFORMATION FOR SEQ ID NO: 27:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Medgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 36,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: denes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road
                                                                                                                                        TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                               APPLICANT: Ligon, James M. APPLICANT: Hill, Dwight S. APPLICANT: Lam, Steven T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                APPLICANT:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                              STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
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TYPE: amino acid
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                COUNTRY: U.ZIP: 27709
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                                                                                                        ADDRESSEE:
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5. 6117670
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Hill, Dwight Steven
Ryals, John Andrew
Hammer, Phillip E.
                                   USA
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Kirner, Sabine
Young, Thomas R.
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                                                                                                      No. 6117670artis Corporation
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Search completed: February
Job time : 17 secs
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Best Local Similarity
"---hes 6; Conserva
                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-028-934-27
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION UNBER: US 08/729,214
APPLICATION UNBER: US 08/729,214
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-7UN-194
ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1506/CITELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                        TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 370 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                         214 SLARAG 219
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Total number of hits satisfying chosen parameters:
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Maximum DB
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seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
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AAW03681
ABG27228
ABG27519
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AAW95381
ABP42408
                                       AA008731
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              Heparin-binding pr
Antimicrobial pept
Human ovarian anti
Human cancer assoc
Long term potentia
Novel human diagno
Novel human diagno
Human polypeptide
Human colon cancer
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Human secreted pro
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229	, n	459	230	130	110	93	84	83		83				62	62	62	62			62	62	35 5	118	118	118	118	118	118	118	118	118	90	61	312
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AAU31057	AAC20231	ARG34132	ABG34133	672	AAG32886	AAG34118	AAG32887	AAG44882	070	AAG31871	AAG48690	AAG44883	AAG40788	AAG40704	AAG39476	AAG38861	AAG34119	AAG32888	AAG22753	AAG15348	AAG04311	AA007113	ABG37354	AAM03364	AAM28118	562	AAM67811	541	003	462	'n	2752	2723	AAU30872
Novel human secret		seb4D	an seb4B prote	Zea mays protein f	mays protein		mays	protein	Zea mays protein f	thal	bidopsis thali	mays	mays protein	0		b1dops	mays	mays protein	mays protein	thal	Q.	polypept	eptide	#2046	#2155	de #20	bone m	brain ex	ein #2034	lde #2131	1de #210	1 human	l human diagn	Novel human secret

ALIGNMENTS

AAR48204 RESULT 1

AAR48204 standard; protein; 59 AA.

AAR48204;

New heparin-binding protein - used as treatment of wounds and bone disease WPI; 1994-031824/04. (FARH) HOECHST JAPAN LTD 05-JUN-1992; 05-JUN-1992; 21-DEC-1993. JP05339287-A. Rattus norvegicus Cell growth agent; wound; bone disease; treatment; treating; agent. Heparin-binding protein. 12-JUL-1994 (first entry) 92JP-0145125 92JP-0145125 Ω cell growth agent

The sequence is that of a heparin binding-protein which is useful as a cell growth agent and in the treatment of wounds and bone disease.

Claim 1; Page 3; 4pp; Japanese

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RESULT 2
AAW95381 ID
AAW95381 
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                                                                                                                                                                          Sequences AAW95381-389 represent antimicrobial peptide fragments derived from ubiquicidine. Ubiquicidine or optionally modified peptide fragments of ubiquicidine, may be used for the treatment, diagnosis, or prophylaxis of infections in humans and animals. In particular the products and methods are directed against microbial infections caused by pathogenic Gram-positive Staphylococcus aureus, including antibiotic resistant strains, Listeria monocytogenes, and Gram-negative antibiotic resistant Klebsiella pneumoniae, E. coli, enterococci, and Salmonella typhinuriom bacteria, micro-organisms difficult to treat such as Mycobacterium avium and M. fortuitum, fungi such as Candida albicans, Cryptococcus neoformans, and Aspergillus fumigatis, viruses, in particular enveloped viruses, and parasites such as Trypanosoma cruzi an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubiquicidine; treatment; diagnosis; prophylaxis; infection; microbial; pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus; Listeria monocytogenes; Gram-negative; Klebsiella pneumoniae; E. coli; enterococcus; Salmonella typhinuriom; Mycobacterium avium; M. fortuitum; fungus; Candida albicans; Cryptococcus neoformans; Aspergillus fumigatis; virus; parasite; Trypanosoma cruzi; Taxoplasma gondii.
                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1997;
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                               Local
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l Similarity 100.0%;
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Pred. No.
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             CC ABPA328) and to cDNAs encoding them (ABC4111-ABC5305), and also CC encompasses polypeptides 90% identical and polynucleotides 95% identical CC to the sequences of the invention. The invention additionally relates to CC recombinant vectors and host cells comprising human ovarian antigen CC polynucleotides, antibodies against human ovarian antigens, and the use CC of ovarian antigen polynucleotides and polypeptides in diagnosing, CC treating, prognosing or preventing various ovary and/or breast-related CC metastratic tumours of ovarian or breast origin, reproductive system CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic cyshock syndrome), inflammatory conditions (e.g., mastitis, opphoritis and CC vaginitis), immune disorders (e.g., congenital and acquired conditions related disorders (e.g., anaemia), cardiovascular disorders. CC immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), CC blood-related disorders (e.g., anaemia), cardiovascular disorders and cc respiratory disorders, neurological disorders, gastrointestinal disorders cand urinary system disorders. Ovarian antigen polypeptides and cc undulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which conditions in the therapy, chromosome mapping, in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; cardiovascular disorder; respiratory disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal disorder; urinary system disorder; drug gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuro antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention ABP43228) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID No 3540; 2922pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-147878/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ55485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to 2175 novel human ovarian antigens (ABP41054-to CDNAs encoding them (ABQ54131-ABQ56305), and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO:3540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidibetic; antiasthmatic; antirheumatic; antiarhritic; antiviral; antidibetic; antiasthmatic; antiarhritic; antiarhritic; antiarhritic; antiarhritic; antiarhritic; antiarhritic; coagulant; nootropic; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection;
                                              antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions.
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                                                                                                                                                                                                           AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 1568-1569; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
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                            Polynucleotides, polypeptides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer associated gene; cancer antigen; detection;
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59; Consert
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disease; drug
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   be used
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                            agonists and
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                               antagonists from
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by activating
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                             This is the sequence of a long term potentiation inducing peptide isolated from mice brains by centifugation, extraction, dialysis, reverse phase HPLC and gel filtration chromatography (Sephadex C-25). The peptide is useful for diagnosis and treatment of senile dementia e.g. cerebrovascular or Alzheimer's dementias.
                                                                                                                                                                                                                                                                                                                                                         A long-term potentiation inducing peptide and treatment of senile dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Long
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                    Claim 1; Page 6;
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-368226/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JР08176193-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebrovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW03681 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112
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_
                    KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          term potentiation inducing peptide; mouse; brain; senile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 170
KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potentiation inducing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                          41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                  7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease
                                                                                             69.5%;
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                                                                                             Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 21;
Pred. No. 4.7e-54;
                                                                               Mismatches
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                                                                                             DB 17; I
1.1e-35;

    useful for

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41
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RESULT 6 ABG27228

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ABG27228 standard; Protein; 108

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RESULT 7
ABG27519
ID ABG2
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AC ABG2
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                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC constraint of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful in medical CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in CC cand to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC Specification, but was obtained in electronic format directly from WIPO at fire uninclinable for this patent did not appear in the printed content of the invention.
                                                                                                                                                            Matches
  ABG27519;
                          ABG27519 standard;
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 57587; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS91415
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #27219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
                                                                                                    69
                                                                                                           20 AKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGDNAN 58
                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                              AKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN
                                                                                                                                                            39;
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                    108
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2000US-0649167.
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                                                                                                                                                                                                                    A,
                          Protein; 108
                                                                                                                                                                     66.1%;
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                                                                                                                                                                    Score 39;
Pred. No.
                         AΑ
                                                                                                                                                                  DB 22; 1
3.2e-33;
                                                                                                                                                      0
                                                                                                                                                                                Length 108;
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RESULT 8
AAO08731
ID AAO0
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AC AAO0
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DT 06-N
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                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and C polymerase (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (C iristore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or guantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical C imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO cat first patent did not appear in the printed CC at first patent in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CC at first patent did not appear in the printed CCC at first patent did not appear in the printed CCC at first pa
                                                                                                                                                                                                                                                                                    Matches
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                                              AA008731;
                                                                                  AAO08731 standard;
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 57878; 103pp; English.
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23-AUG-2000;
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                                                                                                                                                                                                 69
                                                                                                                                                                                                                 20 AKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN 58
                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                           AKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNAN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-639362/73.
                                                                                                                                                                                                                                                                                    39;
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                                                                                                                                                                                                                                                                                                                                                                        108 AA;
                                                                                                                                                                                                                                                                               Conservative
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2000US-0649167.
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                                                                                  Protein; 40
                                                                                                                                                                                                                                                                                                   66.1%;
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                                                                                                                                                                                                                                                                           Score 39; DB; Pred. No. 3.2
0; Mismatches
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                               DB 22;
3.2e-33;
                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                       Length 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutations
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                                                                                                                                                                                                                                                                         Gaps
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06-NOV-2001

(first entry)

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RESULT 9
AAG75965
ID AAG7
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AC AAG7
XX
DT 03-S
XX
DT 03-S
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KW Huma
XX
KW Huma
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KW Huma
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KW Homc
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activity in the diagnosis and/or activity in the diagnosis and or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; lukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                     03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 22623; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                   Human colon cancer antigen
                                                                                                                                                                                                                                                       AAG75965;
                                                                                                                                                                                                                                                                                                         AAG75965 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer, leukaemia,
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                       Homo sapiens
                                                                         colorectal carcinoma;
                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 EKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
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                                                                                              colon cancer; colon cancer antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.7%;
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                                                                            chromosome 11.
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                                                                                                                                                   protein SEQ ID NO:6729
                                                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB Pred. No. 1.7 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
1.7e-31;
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                                                                                                 detection;
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RESULT 10
AAG01569
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-235357/24.
N-PSDB; AAH35370.
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03-NOV-1999;
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                                                                                                                               gene
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                                                                                                  Homo sapiens
                                                                                                                                                                          Human secreted
                                                                                                                                                                                                        06-OCT-2000
                                                                                                                                                                                                                                      AAG01569
                                                                                                                                                                                                                                                                  AAG01569 standard; Protein; 130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                          106 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQ 142
                                                                                                                                                                                                                                                                                                                                                          1 KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQ
                                                                                                                               therapy; chromosome mapping.
                                                                                                                                                5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 8192-8193;
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99US-0163280.
                                                                                                                                                                         protein, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 62.7%; Score 37; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birse
                                                                                                                                               sequence tag; secreted protein; cDNA isolation;
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5.7e-31;
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21-FEB-2000; 2000EP-0200610

06-SEP-2000.

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RESULT 11
AAUJO872
ID AAUJO872
ID AAUJO872
AC AAUJO87
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                                                                                                                                          Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaem
     Nucleic acids encoding a range of human vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                       WPI; 2001-611725/70.
                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                      18-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                     16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted protein #1363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU30872 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards
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)B; AAC01575.
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                                                                                                                                          Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID 5650; 71pp + CD-ROM; English.
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2001US-0770160
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                                                                                                                                             Drmanac
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8d
                               polypeptides,
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                                 useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in cartilage, tendon and/or nerve tissue growth or regeneration; timune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
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Best Local S
Matches 32
                                                                                                                            Claim 20;
                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #27221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 EKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKG 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    supplement;
                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73.
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                                                                                                                            SEQ ID No
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100.0%; Pr
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                                                                                                                         57589; 103pp;
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Pred. No.
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1.9e-25;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and for chrome polymerase chain reaction (PCR) primers, oligomers, and primers (PCR) prime

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RESULT 13
ABG27500
ID 276507
XX ABG27
XX 18-FE
XX 18-FE
XX Human
KW Human
KW Food
XX Homo
XX H
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CC Note: The sequence data for this patent did not appear in the printed constant of the content of the content of the printed content of the content of the printed content of the content of the content of the printed content of the content of the content of the printed content of the content of the content of the printed content of the content of the printed content of the conte
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Best Local
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tag.
                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess blod/versity -
                                                                                                                                                                                                                                         Claim
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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2000US-0649167
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       as expressed sequence tags
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RESULT 14
ABB29449
ID ABB29
XX ABB29
XX ABB29
XX ABB29
XX Human
XW Human
XW Human
XW Human
XW Hopel
QC MAR
ABB29
XX Homo
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Best Local :
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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Pred. No.
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids

New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -

Claim

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NO 12417;

327pp + sequence

listing;

English.

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RESULT 15
ABB34625
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CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the
                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                     27; SEQ
                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #2131
                                                                                                                                                                                                                           Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 AA;
                                                                                                                                                                                                                                                                               2000US-0207456.
2000US-0608408.
2000US-063366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312
                                                                                                                      H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded by human
                                                                                                                                                                                                                         DK,
                                                                                                                   NO 27260; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.5%;
100.0%;
                                                                                                                                                                                                                         Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression;
                                                                                                                                                                                                                         Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28;
Pred. No.
                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                  English
                                            from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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RESULT 16
ABB20035
AC ABB20
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSXGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                         The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one sucl probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          Single
hearts
  Sequence
                                                                                                                                                                                                                                                                                                                                                                            Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB20035 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein #2034 encoded by probe for measuring heart cell gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB20035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                                                                                                                                                                                                                                                                               exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 21805; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234685.
2000US-02346359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heart; microarray; vas
hypertension; cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                            probes for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arrhythmia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                        such
                                                                                                                                                                                                                                                                                               (see
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Query Match Best Local S Matches 28

Similarity

47.5%;

Score 28; Pred. No.

DB 22; 1.3e-21;

Length 118;

Conservative

0;

Mismatches

ç

Indels

0;

Gaps

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AAM55115
ID SAM55
AC AAM55
XX AAM55
AC 
 RESULT 18
AAM67811
ID AAM67
XX
AC AAM67
XX
DT 06-NC
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                                                                                                                                                              밁
                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                        brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
   06-NOV-2001
                                                                     AAM67811
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM55415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM55415 standard;
                                      AAM67811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       بر
                                                                                                                                                            KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                              KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel
                                                                                                                                                                                                                                                                                                          118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000GB-0024263.
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0180312.
                                                                                                                                                                                                                                                                                                                                           the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              댗
                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 118
                                                                                                                                                                                                                                                 47.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27520; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                       118
                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                 Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR;
                                                                                                                                                                                                                                                  DB 22;
1.3e-2
                                                                                                                                                                                                                                                                 Length 118
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>г</u>
О:
                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                0
RESULT 19
AAM15620
ID AAM15620
AC AAM15
XX 12-OC
XX 12-OC
XX Probe
KW Cervi
XX Cervi
XX Homo
XX Homo
XX Homo
XX Homo
PN W0200
PN W0200
PN 09-AU
XX 04-FE
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Query Match
Best Local 9
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
09-AUG-2001
                                      W0200157278-A2
                                                                              Homo sapiens.
                                                                                                                      cervical cancer.
                                                                                                                                       Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                             Peptide #2054 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                         12-OCT-2001
                                                                                                                                                                                                                                                                 AAM15620;
                                                                                                                                                                                                                                                                                                         AAM15620 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO: 28117; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                             56 KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 47.5%; Similarity 100.0%; 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 AA;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
1. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22
1.3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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04-FEB-2000; 2000US-0180312

30-JAN-2001;

2001WO-US00670

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ARMESULT 20
AAM28118
ID AAM28
XX AAM28
AC AAM28
AC AAM28
CDT 17-OC
DE Pepti
XX Probe
KW Probe
KW Genet
XX Homo
OS Homo
XX Homo
XX Homo
PN WO200
PN WO200
PN WO210
PF 30-JI
PF 30-JI
PF 31-SI
PR 21-SI
PR 21-SI
PR 21-SI
PR 04-OC
XX (MOL)
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Best Local (
                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                   AAM28118;
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                                                                                                                                                        30-JAN-2001; 2001WO-US00663
                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                      WO200157272-A2
                                                                                                                                                                                                                                                   genetic disorder.
                                                                                                                                                                                                                                                                                       Peptide #2155
                                                                                                                                                                                                                                                                                                            17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cervical cancer
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                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                   56 KVHGSLARAGKVRGQTPKVAKQEKKKKK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :e: The sequence data for this patent did not form
scification, but was obtained in electronic format
ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                               KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
            SG,
                                                                                                                                                                                                                             sapiens
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zing gene expression in
                                                                                                                                                                                                                                                              microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100
28; Conservative
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                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
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                                                                      ; 2000US-0180312.
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; 2000US-0608408.
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; 2000US-0236359.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                            (first entry)
                                                           2000GB-0024263.
                                                                                                                                                                                                                                                                                    encoded by
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon nucleic acid probes useful
n human cervical epithelial cell:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28;
Pred. No.
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            Rank
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            DR;
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1.3e-21;
                                                                                                                                                                                                                                                                                    placental gene
                                                                                                                                                                                                                                                            diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
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RESULT 2
AAMO 3364
ID AAM
XX AAMO 367
AC AAM
AC PP
DT O9-
PPR O4-
PPR 04-
PPR 04-
PPR 03-
PPR 03-
PPR 03-
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PPR 04
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Best Local S
Matches 28
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by such probe. The probes are useful for measuring human gene expression a human breast sample, where the probe hybridises at high stringency t nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of the probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                            Novel
                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic ac analyzing gene expression in human placenta
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                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                             04 -OCT
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27;
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                                                                                                                                                                                                                                                                                                         2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                      SG,
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                                                                                                                                                                                          27;
                                                                                                                                                                                                                                       single exon nucleic
human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorders.
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                                                                                                                                                                                          SEQ ID No 12104; 322pp;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-06323687.
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2000US-0236359.
2000US-0024263.
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100.0%; Pr
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0; Mismatches
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                                                                                                                                                                                          English
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.3e-21
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d expressing, grave, diagnosing, grave, f

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KW Chrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary disease; pulmonary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                               The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-2002
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                                                                                                                                                                                                                                                                                                           Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                          probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                                                                                                                                                                                                                                                                                                                                                                                   2002-114183/15
                                                                                                                                                                                                                                                         27; SEQ
Also included are a microarray comprising the novel set of
the novel set of probes which hybridise at high stringency
acid expressed in the human lung; measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel
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2000US-236359P.
2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-207456P.
2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                         ID No 27019;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
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                                                                                                                                                                                                                                                      634pp; English.
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Pred. No.
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1.3e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung
 Tang
                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation;
vaccine; peptide therapy; stem cell growth factor; haemator
tissue growth factor; immunomodulatory; cancer; leukaemia;
                                (HYSE-)
                                                                 28-FEB-2000;
18-MAY-2000;
                                                                                                               26-FEB-2001; 2001WO-US04927.
                                                                                                                                                 07-SEP-2001
                                                                                                                                                                              WO200164835-A2
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                               nervous
                                                                                                                                                                                                                                                                                                                              Human polypeptide
                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                               AAO07113;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAO07113 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
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 YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVHGSLARAGKVRGQTPKVAKQEKKKKK 28
                                HYSEQ INC
                                                                                                                                                                                                                                              system disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                               2000US-0515126
2000US-0577409
                                                                                                                                                                                                                                                                                                                              SEQ ID NO
 Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                               arthritis;
   RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28;
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                                                                                                                                                                                                                                               inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                haematopoiesis;
                                                                                                                                                                                                                                                                                              gene therapy;
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RESULT 24
AAG04311
ID AAG04
XX AAG04
XX Prot
XX Prot
KW Prot
KW Prot
KW term
XX Arat
XX Arat
PN EP1
XX O6-
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PR 05-
PR 25-

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Best Local (
     25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

26-APR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

16-APR-1999

17-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activiny, insumomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids a diagnosing and treating disorders -
                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
                                                                                                                                                                                                                                                                                                         25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG04311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG04311 standard; Protein; 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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24; Conserv
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                                                                                                                                                                                                                                                                                                       2000EP-0301439
   99US-0121825

99US-0123180

99US-0125788

99US-0125788

99US-0126264

99US-0127462

99US-0127462

99US-0128234

99US-0128234

99US-0128714

99US-0130077

99US-0130449

99US-0130891

99US-01311449
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g e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d polypeptides, useful for preventing .g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB; Pred. No. 6.8
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
6.8e-18;
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   30-APR-1999
30-APR-1999
04-MAY 1999
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15-JUN-1999
16-JUN-1999
17-JUN-1999
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20-JUL-1999;
20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
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19-JUL-1999;
9908-0132048
9908-0132484
9908-0132485
9908-0132863
9908-0134286
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PR 23-MB
PR 16-AR
PR 16-AR
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PR 11-AR
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99US-0125788.

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99US-0126234.

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99US-0130449.
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                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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RESULT 36
AAG440703
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990S-0130449
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990S-0161993
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	99US-0145218. 99US-0145224. 99US-0145276. 99US-0145913.	9US-01	905-01 905-01	90S-01	010-S06	90S-01	9US-01	90S-01	9US-01	9US-01	10-S06	10-S06	9US-01	90S-01	9US-01	9US-01	905-01	9US-01	90S-01	908-01	9US-01	90S-01	90S-01	90S-01	90S-01	9US-01	9US-01	9US-01	9US-01	9US-01	9US-01	90S-01	90S-01	9US-01	9US-01	905-01	9US-01	90S-01	9US-01	90S-01	
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l Similarity 100.0%;
22; Conservative (
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NO:

39760.

Score 22; Pred. No.

DB 21; 1.8e-15; 0

Length Indels 83

Mismatches

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06-AUG-1999
05-AUG-1999
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29-MAR-1999

16-APR-1999

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16-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

26-APR-1999

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                                                                                               9908-0147935.
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                                                         ch 37.3%; So 1 Similarity 100.0%; I Similarity 0; Conservative 0;
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                                                        Protein;
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                                                                                                                                Score 22; DB; Pred. No. 2.4.0; Mismatches
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       ID NO:
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2.4e-15;
hes 0;
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25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                   Tax interacting protein clone 2; TIP-2; GIPC; antigen; tumour; breast cancer; prostate cancer; monoclonal antibody; 27.B1; 27.F7; thyroid cancer; tetanus toxin; infection; HIV; hanta virus; Ebola; human immunodeficiency virus infection; enzyme dysfunction; hormone dysfunction; autoimmune disease; lupus; rheumatoid arthritis; immune dysfunction; septicaemia; human.
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15-SEP-1:
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14-OCT-1999;
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ABG34132 standard; Protein; 459

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34 RRMQYNRRFVNVVPTFGKKKG

21 54 Similarity 100 21; Conservative

35.6%; 5-100.0%; Pr .-- 0;

Score 21; DB 23; Pred. No. 5.1e-14 0; Mismatches (

.1e-14;

Length 230;

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cancer cells, in a subject. A composition comprising the mab is useful for treating or preventing a condition in a subject who previously cexhibited the condition, where the condition is associated with cancer (thyroid, breast or prostate cancer), tumour (benign), toxin (tetanus, as Hanta virus, HTLV (not defined) I, HTLV II, Human immunodeficiency virus, HTV herpes virus, influenza, Ebola, human papilloma virus, anthrax or Ctryptococcus, Streptococcus, Klebsiella, Escherichia coli, anthrax or Ctryptococcus, enzyme dysfunction (hyperactivity or overproduction of the cenzyme), hormone dysfunction (hyperactivity or overproduction of the bormone), autoimmune disease (lupus, thyroiditis, graft versus host disease, transplantation rejection or rheumatoid arthritis), immune dysfunction (CD) or CD4 mediated), viral antigen, bacterial antigen, rejection of a transplanted tissue, or the condition is septicaemia, sepsis, septic shock, viraemia, bacteraemia, fungaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a monoclonal (mAb) antibody which specifically CC binds and forms a complex with TIP-2 (Tax interacting protein clone 2, also known as GIPC) antigen located on the surface of human cancer cells, CC where mAb binds to the same antigen as monoclonal antibody 27.B1 CC PTA-1599 or 1598, respectively. The mAb is useful for detecting TIP-2 CC antigen bearing cancer cells, for diagnosing cancer in a subject by CC detecting TIP-2 antigen-bearing cancer cells, for detecting TIP-2 antigen-bearing cancer cells for in vivo diagnosis of CC cancer in a subject, for delivering exogenous material to TIP-2 antigen-bearing cancer cells of a human subject, for treating cancer in a human cCC immunohistochemical screening of a tissue section from a tumour sample CC for the presence of TIP-2 antigen in biological fluid, and for monitoring the progression of cancer, where the cancer cells are TIP-2 antigen-bearing cancer cells, for detecting the progression of cancer, where the cancer cells are TIP-2 antigen-bearing cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Fig 41B; 276pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monoclonal antibody which specifically binds and forms complex with TIP-2 antigen located on surface of human cancer cells, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-362353/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCO ) UNIV COLUMBIA NEW YORK
                                            be used in the production of monoclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and treating cancer in a human subject
230
A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalantarov G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rudchenko
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pathway;
promoter;

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The invention relates to a monoclonal (mAb) antibody which specifically calso known as GIPC) antigen located on the surface of human cancer cells, where mAb binds to the same antigen as monoclonal antibody 27.B1 CC where mAb binds to the same antigen as monoclonal antibody 27.B1 CC or 27.F7 produced by hybridoma 27.B1 or 27.F7 produced produced by hybridoma 27.F7 produced by hybridoma 27.B1 or 27.F7 produced by hybridoma 27.F7 produced produced by hybridoma 27.F7 produced p
                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-2000; 2000US-0664958.
                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Fig 41A; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trakht I, Canfield R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-2001; 2001WO-US29242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tax interacting protein clone 2; TIP-2; GIPC; antigen; tumour; breast cancer; prostate cancer; monoclonal antibody; 27.B1; 27.F7; thyroid cancer; tetanus toxin; infection; HIV; hanta virus; Ebola;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human seb4D protein
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                                                                                                                                                                                                  can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dysfunction; septicaemia; human.
                                                            Similarity
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                                  Conservative
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                                                            35.6%;
100.0%;
                                                                                                                                                                                               the production of monoclonal antibodies.
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                                                         Score 21; DB 23; pred. No. 9.3e-1;
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                                  Mismatches
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                                                      9.3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID
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99US-0134370.
99US-0134768.
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99US-0132407.
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                                                                                                    Qy
                                                                                                                                                                                                           The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and in the protein are useful in genetic to explain the proteins. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and continues to requence of novel human secreted proteins of the invention.
                                                                                                                                      Query Match 32.3
Best Local Similarity 100
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 397; 765pp; English.
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611725/70.
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26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted protein #1548.
                                                                                     36 MQYNRREVNVVPTEGKKKG 54
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                                                                       MOYNRREVNVVPTEGKKKG
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                                                                                                                                                                                                           229 AA;
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                                                                                                                                32.2%; Sur
100.0%; Pr
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                                                                                                                                    Score 19; DB 22;
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0; Mismatches 0;
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